



SEQUENCES AND COMPOSITIONS FOR INCREASING
ANTIBODY PRODUCTION

Reilly et al. Attorney Docket P1957R1

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1 GAATTCACCT TCTCCATCT TTGATAAGG AATATACAGC ATGAAAAATC TCATTCTGTA GTTGTATT TT AAGTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAGTTGA AGAGGTATGA AACCTATTC TTATGTCTG TACTTTTAG AGTAACGACT CAACAATAA TTCGAACGGG TTTTCTTTCT TCTCAGCTTA

101 GAACGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGAATTGAT CAGGTAGAGG
CTTGACACAC GGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGGTTTATC TGGTTGTGCG CAACATACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATAGG GAGCTGCTGC GCGATTAGCT AAAGAAGTGA TTGAAGCATC CTCGTACGTA
CCCCGGACAT GCTCCATTTC GGGCTACGCT CGTAAGGACT GCTGCTATGC CTCGAGCAGC CGCTAATGCA TTTCTTCAAT AACTCTGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCAATG AGTTGTACG GCGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTGTAACTA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATACAT AAACATTGAT CATGCGTTCA

401 TCAGGTAAA AGGGTATCTA GAATTATGAA GAAAACATC GCTTTCTTC TTGCACTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACTT CTTTGTGTAG CGAAAGAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTGTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^start STII signal TIR-2 start light chain^

501 CAGATGACCC AGTCCCGAG CTCCTGTCC GCTCTGTGG GCGATAGGT CACCATACC TCAGAGCCA GTCCGACAT CAAGAGCTAT CTGAACCTGT
GTCTACTGG TCAGGGGCTC GAGGACAGG CGGAGACCC CGCTATCCA GTGTAGTGG AGCTCTGGT CAGGCTGTA GTTCTGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTA CTATGCTACT AGTCTGCTG AAGAGTCCC TTCTGCTTC TCTGATCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAT GATACAGTA TCAGAGCAC TTCTCAGGG AAGAGCGAAG AGACCTAGG CAAGACCTCG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G T

701 GGATTACACT CTGACCATCA GCAGCTGCA GCCAGAGAC TTCGCAACTT ATTACTGTCT TCAGCAGGA GAGTCTCCAT GGACATTGG ACAGGGTACC
CCTAATGTGA GACTGGTAGT CGTCAGAGCT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCTGCTT CTCAGAGGTA CCTGTAAACC TGTCCTGATG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGAGA TCAACGAC TCCTGCTGCA CCATCTGTCT TCATCTTCCC GCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACTCT AGTTGCTTG ACACCGAGT GGTAGACAGA AGTAGAGGG CGGTAGACTA CTCGTCACT TTAGACCTTG ACAGAGACAA CACACGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCGAGA GAGGCCAAG TACAGTGAA GTTGATAAC GCCTCCAAT CGGTTAATC CAAGAGAGT GTACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGTTTC ATGTCACCTT CCACCTATTG CGGAGGTTA GCCCATGAG GTCTCTCTCA CAGTGTCTCG TCTGTCTGTT

160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GAGCTGAGC AAAGCAGCT ACAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCTGAGC
CCTGTGCTG ATCTCGAGT CGTCGNGGA CTGCGACTCG TTTGCTGTA TCTCTTTGT GTTTCAGATG CGAGCGCTTC AGTGGTAGT CCCGACTCG

193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

FIG. 2A

DS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

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1001 GGAGCGCACC TACAGCGGCA GCAGCAGCCT GACGCTGAGC AAGCAGACT ACAGAGACT CAAAGTCTAC GCGGCGAAG TCACCCATGA GGGCCCTGAGC
 193 ~~CGGTCGTGG ATGTCGGAGT CGTGGGGA CTGCGACTGG TTTCGTCTGA TGACCTTGT GTTTCAGATG GCGAGCTTC AGTGGGAGT CCCGACTCG~~
 D S T P S L S S T L T M S K A D Y E K H K V Y A C E V ~~P H Q S L S~~

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCTCT ACGCCGAGC CATCGTGGG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
 AGCGGGCAGT GTTCTCGAA GTTGCCCT CTCAATAA ATTTAGGAGA TGGGGCTGC GTAGCACGC TCGAGCCATG GGGCCCTAGA TCGGATTC
 226 S P V T K S F N R G E C O

1201 CTCGTTGCC GCGGGGGT TTTTATGTT GCGACGCGC ATCTGAATG AACTGTGTG GCAGGTAGAA GCTTTGGAGA TTATGTCAC TGCATGCTT
 GAGCAACCG CGGCCGCA AATAACAA CGGCTGGG TAGACTTAC TTGACACAG CGTCCATCTT CGAACCTCT ATAGCAGTG ACGTTACGAA

1301 CGCATATGG CGCAATGA CCAACAGCG TTGATGATC AGTACAGGG GCGCTGTAC GAGTAAAG CCGATGCCAG CATTCCTGAC GACGATACGG
 GCGTTATACC GCGTTTACT GGTTCGCC AACTAATAG TCCATCTCC CCGGACATG CTCATTTCC GGTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGTGG CGATTACGTA AAGAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTCACAG CTGTCTAATA GTTGTACGG CCGAGACTTA
 TCGACGAGCG GCTAATGCAT TTCTCAATA ACTTCGTAGG AGCATCANT TTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGTCTGAT

1501 TAGTCGCTTT GTTTTATTT TTTAATGAT TTGTAATAG TACGCAAGT CACGTAATAA GGTATCTAG AATTATGAG AAAACATCG CTTTCTTCT
 ATCAGCGAA CAAAATAAA AATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCATAGATC TTATATCTT TTTTGTAGC GAAAGAAGA
 M K K N I A F L L
 ^start still signal TIR-2

1601 TGCATCTATG TTCGTTTTT CTATTGCTAC AAACGGTAC GCTGAGTTC AGTGTGTA GTCTGGGT GCGCTGGTGC AGCCAGGGG CTCACTCCGT
 ACGTAGATAC AAGCAAAAG GATAACGATG TTGCGCATG CGACTCCAAG TCGACCACT CAGACGCCA CCGGACCAAG TCGTCCCGC GAGTGAGGCA
 10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R
 ^start heavy chain

1701 TTGCTCTGTG CAGCTTCTG CTTCAATANT AAGGATCT ACATGACTG GTCTGCTAG GCGCCGGTA AGGCGCTGGA ATGGTTGGA TTGATGATC
 AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCGCAT TCCCGGACCT TACCCACCT AACTAATAG
 43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P

1801 CAGAGCAAG CAACAGATC TATGACCGA AGTTCAGGA CCGTGCACT ATAGCGCTG ACAATCCAA AAACACAGCA TACCTGCAGA TGAACAGCTT
 GTCTCGTCC GTTGTGCTAG ATACTGGCT TCAAGTCTT GGCACGCTGA TATTCGAC TGTAAAGTT TTTGTGCTG ATGGAGCTCT ACTTGTGGA
 77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L

1901 GCGTCTGAG GACACTGCC TCTATTATG TGCTGAGAC AGCGCGCTT ACTTCACTA CTGGGTCAA GGAACCTGG TCACGCTC CTCGGCCTCC
 CGCAGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTGGGACC AGTGGCAGAG GAGCCGGAGG
 110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S

2001 ACCAAGGGC CATCGGCTT CCCCTGGCA CCTCTCCA AGAGCACCTC TGGGGGACA GCGGCCCTGG GTCCTCTGT CAAGGACTAC TTCCCCGAAC
 TGGTTCCCG GTAGCCAGAA GGGGACCGT GGGAGGAGT TCTCTGGAG ACCCCCTGT CGCCGGACC CGACGACCA GTTCTGATG AAGGGGCTTG
 143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P

2101 CGGTACCGT GTCGTGAAC TCAGGCGCC TGACAGCGG CGTGACACC TTCCCGCTG TCCTACATC CTCAGACTC TACTCCCTCA GCAGCGTGGT
 GCCACTGCCA CAGCACCTTG AGTCGCGGG ACTGTGCCC GCACGTGTG AAGGGCGAC AGGATGTCAG GAGTCTGAG ATGAGGAGT CGTGACCA
 177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

FIG. 2B

MODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

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2101 CGGTGAAGGT GTCTGGAGC TCAGGCGCC TGACGAGCG CGTGCACACC TTCCCGGCTG TCTTACAGTC CTAGAGACTG TACTCCCTCA GCAGCGTGGT
GCCAGTGCCA CAGCACTTGT AGTCGGGCG ACTGGTCGCG GCACGTGGG AAGGCGGAC AGGATGTGAG GAGTACTGAG ATGAGGAGGT GTCCGACCA
177 V T V S W N S E A L T S G V H T P P A V L Q S S G L Y S L S S V V
2201 GACTGTGCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAAGTGA ATCACAAGCC CAGCAACACC AAGTGGACA AGAAGTTGA GCCCAATCT
CTGACACGGG AGATCGTGA ACCGTGGGT CTGGATGTAG ACGTTCACCT TAGTGTGG GTCTGTGG TTCCACTGT TCTTCACT CGGTTTGA
210 T V P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S
2301 TGTGACAAA CTCACACATG CCCACCTGC CCAGCACTG AACTCTGG GGGACGCTCA GTCTTCTCT TCCGCCAAA ACCCAAGGAC ACCCTCATGA
ACACTGTTTT GAGTGTGTAC GGTGGCAGG GGTGTGTAC GGTGTGTAC CCGTGGACCC CCGTGGACCT CAGAAGGAGA AGGGGGTIT TGGTTCTG TGGGAGTACT
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I
2401 TCTCCCGAC CCTGAGGTC ACATGCTGG TGGTGGAGT GAGGCAGAA GACCTGAGG TCAAGTTCAA CTGTACGTG GACGGCGTGG AGGTGCATAA
AGAGGGCTG GGGACTCCAG TGTAGCCACC ACCACCTGCA CTGGTGCTT CTGGGACTCC AGTTCAGTT GACCATGCAC CTGCGGCACC TCCAGGTATT
277 S R T P E V T C V V D V S H E D P E V K F N W Y V D G V E V H N
2501 TGTCAAGACA AAGCCGCGG AGGACAGTA CACAGCAG TACGCTGG TACGCTCTCT CACGCTCTG CACCAAGACT GGCTGAATGG CAAGGAGTAC
ACGGTTCTGT TCGGCGCCC TCCTGCTCAT GTGTGCTGC ATGCACACC AGTCGACGGA GTGGCAGAC GTGGTCTGA CCGACTTACC GTTCTCTATG
310 A K T K P R E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y
2601 AAGTGAAGG TCTCCAAACA AGCCCTCCA GCGCCATCG AGAAACCAT CTCCAAAGCC AAAGGGCAGC CCGGAGAAC ACAGGTGTAC ACCGTGCCCC
TTCAGCTTCC AGAGTTGTT TCGGGAGGT CCGGGGTAGC TCTTTGTA GAGTTTGG TTTCCTCTG GGGCTCTTGG TGTCCACATG TGGGACGGG
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P
2701 CATCCCGGA AGAGATGACC AAGAACCAGG TCAGCTGTC CTGCTGTC AAAGCTTCT ATCCAGCA CATGCGCTG GAGTGGAGA GCAATGGGA
GTAGGGCCCT TCTCTACTG TTCTTGTCC AGTCGACTG GACGGACCAG TTTCGAAGA TAGGTCGCT GTAGGGCAC CTCACCTCT CGTTACCCGT
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q
2801 GCGGAGAAC AACTACAAGA CCAGCCTCC CGTGTGAC TCGACGCT CTTCTCTCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
CGGCTCTGT TTGATGTTCT GTGCGGAGG GCACGACCTG AGGTGCGGA GGAAGAAGA GATGCTTTC GAGTGGCACC TGTTCGTGTC CACGTCGTC
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q
2901 GGGACGTCT TCTCATGCTC CGTATGTCAT GAGGCTCTGC ACAACACTA CACGAGAAAG AGCCTCTCC TGTCTCGGG TAAATGACA TGCACGGCC
CCCTTGACA AGAGTACGAG GCACTACGTA CTCGAGACG TGTGTGTAT GTGCTCTTC TGGGAGGG ACAGAGGCC ATTTATCTGT ACCTGCGCG
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O
3001 CTAGAGTCCC TAAGCTCGG TTGCGCGCGG CGGTTTTTA TTGTTAACTC ATGTTGACA GCTTATCATC GATAAGCTTT AATGCGTAG TTTATCACAG
GATCTCAGG ATTGCGAGC AACGCGCGC CGCAAAAAT AACAAATTGAG TACAACTGT CGAATAGTAG CTATTCGAAA TTACGCCATC AATAGTGTG
3101 TTAATTTGT AACGCAGTCA GGCACCGTGT ATGAATCTA ACATGCTCT CATGCTCATC CTCGGCACC TCACCTGGA TGTGTAGG ATAGGCTTGG
AATTTAACGA TTGGTCACT CCGTGGCACA TACTTAGAT TGTACGGA GTAGCAGTAG GAGCCGTGGC AGTGGACCT AGACATCCG TATCCGAACC
3201 TTATGCGGT ACTGCGGGC CTCTTGGGG ATATGTCOA TT
AATACGCCA TGACGCGCG GAGAACGCC TATAGAGT AA

FIG. 2C

SEQUENCES AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

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1 GAATTCAACT TCTCCATCT TTGGATAAG AATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTT AAGCTTGCCC AAAAAGAGA AGAGTCGAAT
CCTAAGTTGA AGAGGTATGA AACCTATTCC TTATGTCGTG TACTTTTAG AGTAACGACT CAACAATAA TTGCAACGGG TTTTCTCTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GGTCCATCT TCGAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGGTTTATC TGGTTGTCCG CAACTAATA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCGGATGCCA GCATTCTGTA CGAGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTACGTA
CCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGC CGCTAATGCA TTCTCTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCTATA AGTTGTCACG GCGGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAATGTA TTGTAACTA GTACGCAAGT
TTTTCATTA GAAAGTTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAA AAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGATATC GCATTCTCTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAACGCTA CGCTGATATC
AGTGCAATTT TCCCATAGAT CTTAATACTT CTTCTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^still signal TIR -1 ^Light chain

501 CAGTTGACCC AGTCCCGAG CTCCTGTCC GCCTGTGTG GCGATAGGT CACATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAACCTGGT
GTCAACTGGG TCAGGGGCTC GAGGGACAGG CCGTATCCCA GTGCTAGTGG AGTCCGCTT CAGTCCCTATA ATCGTTGATA AATTGACCA

26 Q L T Q S P S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGAAAG GCTCCGAAAG TACTGATTTA CTTCACTCC TCTCTCCACT CTGAGTCCC TTCTGCTTC TCTGATCCG GTTCTGGGAC
TAGTTGCTTT TGGTCTTTT CGAGGCTTTC ATGACTAAT GAAGTGGAGG AGAGAGTGA GACCTCAGG AAGACGAG AGACCTAGG CAAAGACCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G T

701 GGAATTCAC CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGCA ACAGTATAGC ACCGTGCGGT GGACGTTGG ACAGGGTACC
CCTAAGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGT TGTATATCG TGGCACGCA CCTGCAAAACC TGTCCCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGGAGA TCAACGAC TGTGCTGCA CCATCTGCT TCACTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACAGTGGAA GGTGGATAAC GGCCTCCAAT CGGTTAACTC CCAGGAGAGT GTACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGTTTC ATGTCACCTT CCACCTATTG CCGGAGTTA GCCATTGAG GGTCTCTCTCA CAGTGTCTCG TCTGTGCTT

160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAGCAGACT ACGAGAACA CAAAGTCTAC GCTGCEAAG TCACCCATCA GGGCCTGAGC
CCTGCTGGG ATGTCGAGT CGTCTGGGA CTGCGACTCG TTGCTCTGA TGTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGGTAGT CCGGACTCG

193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

FIG. 4A

ODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION

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1001 GGACACACAC TACAGCCTTA GCAGACCCG GACGCTGAGC AGGCGAGCT ACAGAGACA CAAGAGTAC GCTCTGCGAG TACACCAAT GGGCCTGAGC
CCTCTGCTGG ATGCTGGAGT CGTCTGCGA CTGCGAGCTG TTCTGCTGTA TCTCTTTGT GTTCTAGATG CGAGGCTTC AGTCTAGT CCAGACTCG
193 D S T Y S L S S T L T L S K A S Y E K H K V Y K C E V T H Q G L S
1101 TCGCCCTCA CAAGAGCTT CAACAGGGA GAGTCTTAAT TAACTCTCT AGCCGAGC CATCTGGG AGCTCGGTAC CCGGGATCT AGGCTTAACG
ACGGGCGAGT GTTCTCGAA GTTCTCCCT CTCACATTA ATTAGGAGA TCGGCGCTGC GTAGCACCG TCGAGCCATG GCGCCCTAGA TCGGATTC
226 S P V T K S F N R G E C O
lambda to terminator^
1201 CTCGCTGCC GCGGGCGTT TTTTATGTT GCGAGCGGC ATCTGAATG AACTGTGTC GCAGTAGAA GCTTTGAGA TTATGTCAC TGAATGCTT
GAGCCACGG CCGCCCGCAA AAAATRAAA CGGCTGCGG TAGAGCTTAC TTACACACG CGTCCATCTT GGAACCTCT AATAGCAGT ACCTTACGA
1301 CGCAATATG CGCAAAATGA CCAACAGGG TTGATTAATC AGGTAGAGG GCGCTGTATC GAGTAAAGC CGATGCCAG CATTCCTGAC GACGATACGG
GCTTATACC GCGTTTACT GGTGTGCGC AACTAATAG TCCATCTCC CCGGACATG CTCCATTTG GCTACGGTC GTAGGAGTGT CTGCTATGCC
1401 AGTCTCTGG CGATTAGTA AAGAATTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACG CTGTCTATAA GTTGTACGG CCGAGACTTA
TCGAGGACG GCTAATGCAT TTCTCAATA ACTTGTAGG AGCATCAT TTCTAATTAG AAAAGTTGTC GACATATTT CAACAGTGCC GGTCTGAAT
1501 TAGTCGCTTT GTTTTATTT TTTAATGTA TTGTAATAG TACGCAAGT CACGTAATAA GGTATCTAG AATTAGAG AAGAATATG CATTTCTTCT
ATCAGCGAA CAAAATATA AATATACATA AACATGATC ATGCGTTCAA GTGCTATTT CCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
M K K N I A F L L
^STII signal TIR-1
1601 TGATCTATG TTCGTTTTT CTATGCTAC AAACGGTAC GCTGAGTTC AGTGTGTA GTCTGCGGT GGTCTGTGTC AGCCAGGGG CTCATCCCT
ACGTAGATAC AAGCAAAA GATAAGGATG TTGCGCATG CGACTCAAG TCGACCAT CTAGACCGCA CCGGACACG TCGTCCCCC GAGTGAGGA
10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R
^start heavy chain
1701 TGTCTCTG CAGCTTCTG CTATCTCTC ACCACTATG GPATAACTG GTCTGCTAG GCTCGGTAG AGGCGCTGGA ATGGTTGA TGGATTACA
AACAGGACAC GTCAAGAC GATATGGAAG TGTGTATAC CATATTGAC CCAGGCTGTC GCGGCGCAT TCCCGGACCT TACCAACCT ACCTAATGT
43 L S C A A S G Y T F T N Y G I N W V R Q A P G K G L E W V G W I N T
1801 CCTATACCG TGAACCGACC TATGCTGCG ATTTCAAGC TGTCTTACT TTTTCTTATG ACCTCTCAA AAGCAGACA TACTGACGA TGAACAGCT
GGATATGCC ACTTGGCTG ATACGAGCC TAAAGTTTGC AGCAAGTGA AAGAATACT TGTGAGGT TGTGTGCTGT ATGACGCTCT ACTTGTGGA
77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L
1901 GCGGCTGAG GACTGTGCG TCTATTACTG TGCAGATAC CCGCACTAT ATGTGAACGA GCGAAGAGC CACTGTATTT TCGACGCTGT GGTCAAGGA
CGCGGACTC CTGTGACGC AGATAATGAC ACCTTTCTATG GCGGTGATTA TACACTGTCT CGCTTTCTG GTGACCATTA AGCTGACAGC CCCAGTTCTT
110 R A E D T A V Y Y C A K Y P H Y Y V N E R K S H W Y F D V W G Q G
2001 ACCCTGGTCA CGTCTCTC GGCCTCCAC AAGGCGCAT CGTCTTCCC CTGTGACCC TCTTCAAGA GCACCTCTG GGGCAGACG GCGCTGGCT
TGGACCACT GGCAGAGGAG CCGGAGGTG TTCCCGGGA GCCAAGAGG GACCGTGG AGGAGTTCT CGTGAAGAC CCGTGTGCG CCGGACCGA
143 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C
2101 GCTGTGTC AAGACTTTC CCGAAGCGG TGACGTGTC GTGAATCTA GCGGCGCTGA CAGCGGCTG GCACACTTC CCGGCTGTCC TACAGTCTC
CGGACCACTT CCGTATGAAG GCGCTTGGC ACTGCCACAG CACTTGAAT CCGCGGACT GTGCGCGCA CGTGTGAAG GCGGACAGG ATGTGAGG
177 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S

FIG. 4B

2101 GCTGTGCAA GGAATCTATC CCGAAGCCGG TGAAGTGTG GGCAGCTTCA GGCAGCTTCA GGCAGCTTCA GGCAGCTTCA GGCAGCTTCA GGCAGCTTCA
CGGACCAATT CCTGAGGAG GGGCTTGGCC ACTGACACAG CACTTGTAGT CCGGGGACT GGTGGGCA CAGTGTGAG GGCAGCTTCA GGCAGCTTCA GGCAGCTTCA
177 L V K D Y F P E P V T V S W N S S A L T S G V H F P A V L Q S S
2201 AGGACTTAC TCCCTCAGCA GCGTGTGAC TGTGCTCTT AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGATC ACAAGCCAG ACAAGCCAG CAACACCAAG
TCCTGAGATG AGGAGTCTG CGCACCACTG ACACGGGAGA TGCTGGAACC CGTGGGCTG GATGTAGAG ITGCACTTAG TGTTCGGGTC GTTGTGTTTC
210 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K
2301 GTGGACAAGA AAGTTGAGCC CAAATCTTGT GACAAACTC ACATGTCCTT CCGGACCTCC ACCTGTCGCA GCACCTGAAC TCCTGAGGGG ACCGTGAGTC TTCTCTTCTC
CACCTGTTCT TTCAACTCGG GTTTAGAAC CTGTTTGTAG TGTGTAGGG TGGACAGGGT CGTGGACTTG AGGACCCCTC TGGCAGTCCAG AAGGAGAAG
243 V D K K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P
2401 CCCCAGAAC CAGGACACCC CTGATGATCT CCGGACCTCC TGAGTCACTA TGGTGTGTTG TGGAGGTGAG CCACGAGTAC CCGTCTTCTC GGTCTCTGAC
GGGTTTGTG GTTCTGTGTTG GAGTACTAGA GGGCTGTGGG ACTCAGTGT ACACCAACC ACCTGCTTCTG GGTCTTCTG GGTCTTCTG TCAAGTTGAC
277 P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W
2501 GTAGTGGAC GCGTGTGAGG TGCATAATGC CAAGACAAG CCGCGGAGG AGCAGTACAA CAGCAGTAC CCGTGTGTTA GCGTCTTCTC GGTCTCTGAC
CATGACCTG CCGCACCTCC AGTATTACG GTTCTGTTC GCGGCTCTC GTTGTGTTG TGGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
310 Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H
2601 CAGGACTGC TGAATGGCAA GGAGTACAAG TGAAGTGTCT CCAACAAAG CCTCCAGCC CCGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
GTCTGTGAGG ACTTACCGTT CCTCATGTT CCGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
343 Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R
2701 GAGAACCAACA GTGTGACACC CTGCCCCCAT CCGGAGGAGA GATGACCAAG AACCAAGTCA GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
CTCTGTGTTG CCACATGTG GACGGGGTA GGGCCCTTCT CTATGTTTC TTGTTCCAGT CCGACTGAGC GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
377 E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I
2801 CCGGTGTGAG TGGAGAGCA ATGGGAGCC GGAGACAAC TACAGACA CCGTCTCCGT GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
GCGGCACCTC ACCCTCTGT TACCGTCTG CCTCTGTG ATGTTCTGT GCGAGGGCA CCGACTGAGG CTGCGGAGA AGAAGAGAT GTCGTTCGAG
410 A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L
2901 ACCGTGGACA AGAGCAGGTG GCAGCAGGG AACGTCTTCT CATGCTCGT GATGATGAG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
TGGCACCTGT TCTGTTCCAC CGTGTCTCC TGGAGAAGA GTACGAGCA CTACGATCTC CGAGAGTGT TGTGTGTTG GGTGTGTTG GGTGTGTTG GGTGTGTTG
443 T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S
3001 CTCGGGTAA ATAAGCATGC GACGGCCCTA GATCCCTTA CCGTGTGTTG CCGCGGGG TTTTATTG TTAAGTATG TTTGACAGT TATCATCAT
GAGGCCATT TATTCGTACG CTGCGGGAT CTCAGGAT GCGAGCCAAC GCGGCCCCG AAAAAATAAC AATTGAGTAC AAAGTGTGCA ATAGTAGCTA
477 P G K O
*lambda terminator
3101 AGCTTTAAT GCGGTAGTT ATCACAGTTA AATTGCTAAC GAGTGTGAG ACCGTGTATG AAATCAACA ATGCGTCTAT GGTCTCTCTC GGCACCGTCA
TTGAAATTA GCGCATCAA TAGTGTCAAT TTAAGATTG CCGTGTGTTG TGGACATAC TTGATTTGT TACGCGAGTA GCAGTAGGAG CCGTGGCAGT
3201 CCTGTGATGC TGTAGGCATA GCGTTGGTTA TGGCGGTACT GCGGGGCTC TTGCG
GGGACCTAC ACATCCGTAT CCGAACCAAT ACGGCCATGA CCGCCCCGAG ACGC

FIG. 4C

METHODS AND COMPOSITIONS FOR INCREASING
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3201 ~~CCCTGATGC TGTAGGCTAT GCGTTGTTA TCCCGTACT GCGGGGCTC TTGCG~~
~~GGACCTACG ACATCCGTAT CCGACCAAT ACGGCGATGA CCGGCGGAG AACGC~~

FIG. 4D

1 GAATTCAACT TCTCCATCT TGGATAAGG AATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GGGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTGCG CAACATACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCTATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTTATT TTTTAAATGTA TTTGTAACATA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAATAAA AAAATTACAT AACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTCTTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCAATTT TCCCATAGAT CTTAATACCT CTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
STII Signal Sequence TIR-1 Anti-Tissue Factor Light Chain

501 CAGATGACCC AGTCCCCGAG CTCCTGTGCC GCGATAGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAAGTGGT
GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S R S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCCCTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCCTCAGG AAGAGCGAAG AGACCTAGG CAAGACCCCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCCCAACTT ATTACTGTCT TCAGCACGGA GACTCTCCAT GGACATTTGG ACAGGGTACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCTT CTCAGAGGTA CCTGTAAACC TGTCCCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

FIG. 1A

801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCACTCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG
126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L
901 TGAATAACTT CTATCCAGA GAGGCCAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CCGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGGTTT CACCTATTG CCGGAGGTTA GCCCATTCAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K
1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGGGAAG TCACCCATCA GGGCCTGAGC
CCTGCTGTGG ATGTGGAGT CGTCTGGGA CTGGGACTCG TTTCGCTGA TGTCTTTGT GTTTCAGATG CCGACGCTTC AGTGGGTAGT CCCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCTCT ACGCCGGAGC CATCTGGTAC CCGGGGATCT AGGCCTAAGC
AGCGGGCAGT GTTCTCGAA GTTGTCCCT CTCACAATTA ATTTAGGAGA TCGGCCCTGC GTAGCACCGC TCGAGCCATG GCGCCCTAGA TCCGGATTGC
226 S P V T K S F N R G E C O
1201 CTCGGTTGCC GCGGGCGTT TTTTATTGTT GCCGACGCG ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TCGAATGCTT
GAGCCAACGG CCGCCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTTAC TTGACACAGC CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA
1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCTTGAC GACGATACGG
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGGACATG CTCCATTTCC GGCTACGGTC GTAAGGACTG CTGCTATGCC
1401 AGCTGCTGG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACCG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAAATTAG AAAAGTTGTC GACAGTATT CAACAGTGCC GGCTCTGAAT
1501 TAGTGCCTTT GTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGTATCTAG AATTATGAG AAGAATATCG CATTCTTCT
ATCAGCGAAA CAAAAATAA AAATTACATA AACATTGATC ATCGGTTCAA GTGCATTTT CCCATAGATC TTAATCTTC TTCTATAGC GTAAAGAAGA
M K K N I A F L L
^STII Signal Sequence TIR-1

FIG. 1B

1601 TGCATCTATG TTGGTTTTTT CTATTGCTAC AAAGCGGTAC GCTGAGGTTT AGCTGGTGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGG CTCACCTCCGT
ACGTAGATAC AAGCAAAAA GATAACGATG TTTGGCGATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCAGG TCGGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R

*Anti-Tissue Factor Heavy Chain

1701 TTGTCTCTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCACTG GTCCGCTCAG CCCCCGGTA AGGGCCTGGA ATGGGTTGGA TTGATTGATC
AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCAGTC CCGGCCCCAT TCCCGACCT TACCCAACT AACTAACTAG
43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P

1801 CAGAGCAAGG CAACAGCATC TATGACCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT
GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGGCAG TGTAAAGTT TTTGTGTCGT ATGGACGTCT ACTGTGCGGA
77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L

1901 GCGTGTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCGCTT ACTTCGACTA CTGGGGTCAA GGAACCTGG TCACCGTCTC CTCGGCCTCC
CGCACGACTC CTGTGACGGC AGATNATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTGGGACC AGTGGCAGAG GAGCCGGAGG
110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S

2001 ACCAAGGGCC CATCGGTCTT CCGCTGGCA CCTCTCTCA AGAGCACCTC TGGGGCACA GCGGCCCTGG GTCGCTGGT CAAGGACTAC TTCCCCGAAC
TGTTTCCCGG GTAGCCAGAA GGGGACCGT GGGAGGAGT TCTCGTGGAG ACCCCGCTGT CGCCGGGACC CGACGGACCA GTTCTGTATG AAGGGGCTTG
143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P

2101 CCGTGACGGT GTCGTGGAAC TCAGGGGCCC TGACCAGCGG CGTGACACC TTCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
GCCACTGCCA CAGCACCTTG AGTCCGCGG ACTGGTCCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCTGTAG ATGAGGAGT CGTCGCACCA
177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

2201 GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA AGAAAGTTGA GCCCAAATCT
CTGACACGGG AGATCGTCCA ACCCGTGGT CTGGATGTAG ACGTTGCACCT TAGTGTTCGG GTCGTTTGGG TTCCACCTGT TCTTCACT CGGGTTTAGA
210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S

2301 TGTGACAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCTCTGG GGGACCGTCA GTCTCTCTCT TCCCCCAA ACCCAAGGAC ACCCTCATGA
ACACTGTTTT GAGTGTGTAC GGGTGGCAGG GGTGTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGTTTT TGGGTTCTTG TGGGAGTACT
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I

FIG. 1C

2401 TCTCCCGGAC CCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGTACGTG GACGGCGTGG AGGTGCATAA
AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCTT CTGGGACTCC AGTTCAAGTT GACCATGCAC CTGCCGCACC TCCACGTATT
277 S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N
2501 TGCCAAGACA AAGCCGCGG AGGAGCAGTA CAACAGCAGC TACCCTGTGG TCAGCGTCTT CACCGTCTCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
ACGGTCTGT TTCGGGCCCC TCCTCGTCTAT GTTGTCTGTC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCTCTGA CCGACTTACC GTTCTCTCATG
310 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y
2601 AAGTGCAGG TCTCCAACA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC
TTCACGTTC AGAGTTGTT TCGGGAGGTT CCGGGGTAGC TCTTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTTGG TGTCCACATG TGGGACGGGG
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P
2701 CATCCCGGGA AGAGATGACC AAGAACCAAG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATGCCCGTG GAGTGGGAGA GCAATGGGCA
GTAGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGACTG GACGGACCAG TTTCGGAAGA TAGGTCGCT GTAGGGGCAC CTCACCTCT CTTACCCGT
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q
2801 GCCGAGAAC AACTACAAGA CCAAGCTCC CGTGTGGAC TCCGACGGCT CCTTCTTCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
CGSCTCTTG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGNAGGA GATGTCGTT CAGTGGCACC TGTCTCTGTC CACCGTCGTC
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q O
2901 GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGAGAGAG AGCCTCTCCC TGTCTCCGG TAAATAAGCA TCGCAGCGCC
CCCTTGACAG AGAGTACGAG GCACTACGTA CTCGAGAGAG TGTGTGTAT GTGCTCTTC TCGGAGAGGG ACAGAGGCCC ATTTATTCGT ACCCTGCCCG
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O
3001 CTAGAGTCCC TAACGCTCGG TTGCCGCGG GCGTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG
GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAT AACAAATTGAG TACAACCTGT CGAATAGTAG CTATTGAAA TTACGCCATC AAATAGTGT
3101 TTAATTGCT AACGCAGTCA GGCACCGTGT ATGAATCTA ACAATGCGCT CATGCTCATC CTCGGCACCG TCACCTCTGA TGTGTAGGC ATAGGCTTGG
AATTAAACGA TTGCGTCACT CCGTGGCACA TACTTTAGAT TGTACGCGA GTACAGTAG GAGCCGTGGC AGTGGGACCT ACGACATCCG TATCCGAACC
*Start Tet Resistance Coding Sequence
3201 TTATGCCGT ACTGCCGGC CTCTTGCGG ATATCGTCCA TTCCGACAGC ACTATGGCGT GCTGTAGCG CTATATGCGT TGATGCAATT
AATACGGCCA TGACGGCCCG GAGAACGCCC TATAGCAGGT AAGGCTGTCG TAGCGGTGAG TGATACCGCA CGACGATCGC GATATACGCA ACTACGTTAA

FIG. 1D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GGC AAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC CGGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGGTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCACTA
CCCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTC AACA GCTGTCAFAA AGTTGTCAAG GCCGAGACTT ATAGTCGCTT TGT TTTTATT TTTTAATGTA TTTGTAAC TA GTACGCAAGT
TTTTC AATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAA AATTA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGTATCTA GAATTATGAA GAAAAACATC GCTTTCTCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACTT CTTTTTGTAG CGAAAAGAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGGGCAT CGGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^start STII signal TIR-2 start light chain^

501 CAGATGACCC AGTCCCGGAG CTCCTCTGTC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGAGCCA GTCGCGACAT CAAGAGCTAT CTGAACCTGGT
GTCTACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCTCGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTCGTG AAGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GATACGATGA TCAGAGCGAC TTCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAGAC TTGCGAACTT ATTACTGTCT TCAGCACGGA GAGTCTCCAT GGACATTTGG ACAGGGTACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGCTCTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCTCT CTCAGAGGTA CCTGTAAACC TGTCCCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGGAGA TCAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

FIG. 2A

901 TGAATAACTT CTATCCGAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGTAATC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CGGAGAGTTA GCCCATTTAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACAGAGAAACA CAAAGTCTAC GCCTGCCAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTCGAGT CGTCGTGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CGGACGCTTC AGTGGTAGT CCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTTAAT TAAATCTCTT AGCCGGAGC CATCGTGGG AGCTCGGTAC CCGGGATCT AGGCCTAACG
AGCGGGCAGT GTTCTCGAA GTTGTCCCT CTCACAAATTA ATTTAGGAGA TCGGCGCTGC GTAGCACCGC TCGAGCCATG GGCCCTCTAGA TCCGGATTGC
226 S P V T K S F N R G E C O

1201 CTCGGTTGCC GCGGGCGTT TTTTATTGTT GCGGACGGC ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTAC TGCAATGCTT
GAGCCAAACGG CGGCCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCAATATGG CGCAAAATGA CCAACACGG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGTAAAGC CCGATGCCAG CATTCCTGAC GAGCATACGG
GGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTTC GGCTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAAGTA AAAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACGG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT

1501 TAGTCGCTTT GTTTTATTT TTTAATGTAT TTGTAACTAG TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAAACATCG CTTTCTCTCT
ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCAATTTT CCCATAGATC TTAATACTTC TTTTGTAGC GAAAAGAAGA
1 M K K N I A F L L
^start STII signal TIR-2

1601 TGCATCTATG TTCGTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTTT AGCTGGTGA GTCTGGCGGT GGCCTGTGTC AGCCAGGGGG CTCACCTCCGT
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGGCGATG CGACTCCAAG TCGACCACTT CAGACCGCCA CCGGACCCAG TCGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
^start heavy chain

FIG. 2B

1701 TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGGAGTACT ACATGCAC TGTCGGCTGAG GGTCCGCTCAG GCGCCGGGTA AGGGCCTGGA ATGGGTGGA TTGATTGATC
AACAGGACAC GTCGAAGACC GAAGTTATAA TTCTCTATGA TGTACGTGAC CCAGGCAGTC CCGGGCCCAT TCCCGGACCT TACCCAACCT AACTAACTAG
43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P

1801 CAGAGCAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT
GTCTGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCCGAC TGTAAAGGTT TTTGTGTCGT ATGGACGTCT ACTTGTGCGA
77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L

1901 GCGTGTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCCTGG TCACCGTCTC CTCGGCCTCC
CGCAGGACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTGGGACC AGTGGCAGAG GAGCCGGAGG
110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S

2001 ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGTT CAAGGACTAC TTCCCCGAAC
TGTTCCCGG GTAGCAGAA GGGGACCGT GGGAGGAGT TCTCGTGAG ACCCCCGTGT CCGCGGACC CGACGGACCA GTTCTGTATG AAGGGGCTTG
143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P

2101 CGGTGACGGT GTCGTGGAAC TCAGGGCGCC TGACCAGGG CGTGACACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT
GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCTGAG ATGAGGGAGT CGTCGCACCA
177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

2201 GACTGTGCCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGACA AGAAAGTTGA GCCCAAATCT
CTGACACGGG AGATCGTGA ACCCGTGGT CTGGATGTAG ACGTTGCACT TAGTGTGG GTCTGTTGG TTCCACCTGT TCITTCAACT CGGGTTTGA
210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S

2301 TGTGACAAA CTCACACATG CCCACCGTGC CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCTCT TCCCCCACA ACCCAAGGAC ACCCTCATGA
ACACTGTTTT GAGTGTGTAC GGTGTGCACG GGTGTGCAC TTGAGACCC CCCTGGCAGT CAGAAGAGA AGGGGGTTT TGGGTCTCTG TGGGAGTACT
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I

2401 TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCAGAA GACCCTGAGG TCAAGTTCAA CTGTACGTG GACGGCGTGG AGGTGCATAA
AGAGGGCCTG GGGACTCCAG GTAGGCAC ACCACCTGCA CTGGTGCTT CTGGACTCC AGTTCAAGTT GACCATGCAC CTGCGGACCC TCCACGTATT
277 S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N

FIG. 2C

2501 TGCCAAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCAGC TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC
ACGGTTCTGT TTCGGCGCCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCTGA CCGACTTACC GTTCCTCATG
310 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y

2601 AAGTGCRAAG TCTCCAACAA AGCCCTCCCA GCGCCCATCG AGAAAACCAT CTCCAAGGCC AAAGGCAGC CCGGAGAACC ACAGGTGTAC ACCCTGCCCC
TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTGGTA GAGGTTTCGG TTTCCCGTCG GGGCTCTGG TGTCACATG TGGGACGGGG
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P

2701 CATCCCCGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ATCCCAGCGA CATGCCCGTG GAGTGGGAGA GCAATGGGCA
GTAGGGCCT TCTCTACTGG TTCTTGGTCC AGTCGGAAGT GACGGACCAG TTTCGGAAGA TAGGTCGCT GTAGCGGCAC CTCACCTCT CATTACCGT
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q

2801 GCCGGAGAAC AACTACAAGA CCACGCCTCC CGTGCTGGAC TCGACGGCT CTTCTTCTCT CTACAGCAAG CTCACCGTGG ACAAGAGCAG GTGGCAGCAG
CGGCTCTTGG TTGATGTTCT GGTGCGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTT CAGTGGCACC TGTCTCGTC CACCGTCGTC
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q

2901 GGGAAAGTCT TCTCATGCTC CGTGATGCT GAGGCTCTGC ACAACCACTA CAGCAGAAG AGCCTCTCCC TGTCTCCGG TAAATAAGCA TGGGACGGCC
CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCCGAGACG TGTGCTGAT GTGCGTCTTC TCGGAGAGGG ACAGAGGCC ATTTATTCTG ACGTGGCCGG
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O

3001 CTAGAGTCCC TAACGCTCGG TTGCCGCGCG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG
GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAACCTGT CGAATAGTAG CTATTGAAA TTACGCCATC AATATGTC

3101 TTAANTTGCT AACGCAGTCA GGCACCGTGT ATGAAATCTA ACAATGCGCT CATCGTCATC CTCGGCACCG TCACCCCTGA TCGTGTAGGC ATAGGCTTGG
AATTTAACGA TTGCGTCACT CCGTGGCACA TACTTTAGAT TGTTACGCGA GTAGCAGTAG GAGCCGTGGC AGTGGGACCT ACGACATCCG TATCCGAACC

3201 TTATGCCGGT ACTGCCGGGC CTCTTGGGG ATATCGTCCA TT
AATACGCCA TGACGGCCCG GAGAACGCC TATAGCAGGT AA

FIG. 2D

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1 GAATTCAACT TCTCCATACT TTGGATAAGG AATATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CCGGTTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCGATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGC CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCAATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAAC TA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CCGCTCTGAA TATCAGCGAA ACAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAA AGGTATCTA GAATTATGAA GAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACCT CTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
M K K N I A F L L A S M F V F S I A T N A Y A D I
Anti-VEGF Light chain*

501 CAGTTGACCC AGTCCCCGAG CTCCTGTGCG GCGATAGGGT CACCATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAAACTGGT
GTCAACTGGG TCAGGGGCTC GAGGACAGC GCGATACACC CGCTATCCCA GTGCTAGTGG ACCTGCGGTT CAGTCCTATA ATCGTTGATA AATTTGACCA

26 Q L T Q S P S S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTTCACTCC TCTCTCCACT CTGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTT ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G S G T

701 GGATTTCACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTCA ACAGTATAGC ACCGTGCGGT GGACGTTTGG ACAGGTTACC
CCTAAAGTGA GACTGGTAGT CGTCAGACGT CCGTCTTCTG AAGCGTTGAA TAATGACAGT TGTATATCG TGGCAGCGCA CCTGCAAAACC TGTCCTCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGGAGA TCAACGAAC TGTGGTGA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

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FIG. 3A

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACACTGGA GGTGGATAAC GCCCTCCAAT CCGGTAAC TC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGTCT CTCCGGTTTC ATGTACCTT CCACCTATTG CCGGAGGTTA GCCCATGAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K
1001 GGACAGCACC TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGGGAG TCACCCATCA GGGCCTGAGC
CCTGCTGTGG ATGTGGGAGT CGTCGTGGGA CTGGCACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CCGACGCTTC AGTGGGTAGT CCGGCACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAT TAAATCTCT ACGCCGGAGC CATCGTGGG AGCTCGGTAC CCGGGGATCT AGGCCTAACG
AGCGGGCAGT GTTCTCGAA GTTGTCCTCT CTCACAATTA ATTTAGGAGA TGCGGCTGCG GTAGCACCGC TCGAGCCATG GGGCCCTAGA TCCGGATTGC
226 S P V T K S F N R G E C O
1201 CTCGGTTGCC GCGGGCGTT TTTTATTGTT GCCGACGCG ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
GAGCCACCG CCGCCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA
1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGCGACATG CTCCATTTCC GGTACGGTC GTAAGGACTG CTGCTATGCC
1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACCG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTTCAATTAG AAAAGTTGTC GACAGTATT CAACAGTGCC GGTCTGAAT
1501 TAGTCGCTTT GTTTTATTT TTTAATGTAT TTGTAAGTAG TAGGCAAGTT CACGTAAAAA GGTATCTAG AATTATGAAG AAGAATATCG CATTTCTTCT
ATCAGGAAA CAAAAATAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
1 M K K N I A F L L
^STII Signal TIR-1
1601 TGACTCTATG TTCGTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTC AGCTGGTGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACT CAGACCGCCA CCGGACCCAG TCGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
^Anti-VEGF Heavy Chain

FIG. 3B

1701 TTGTCCTGTG CAGCTTCTGG CTACGACTTC AGCAGCTACG GTATGAACTG GGTCGGTCAG GCCCGGGTA AGGCGCTGGA ATGGGTTGGA TGGATTAACA
AACAGGACAC GTCGAAGACC GATGCTGAAG TCGGTGATGC CATACTTGAC CCAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT ACCTAATTGT
43 L S C A A S G Y D F T H Y G M N W V R Q A P G K G L E W V G W I N T
1801 CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCGTTTCACT TTTTCTTTAG ACACCTCCAA AAGCACAGCA TACCTGCAGA TGAACAGCCT
GGATATGGCC ACTTGGCTGG ATACGACGCC TAAAGTTTGC AGCAAGTGA AAAGAAATC TGTGGAGTT TTCGTGTCGT ATGGACGTCT ACTTGTTCGGA
77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L
1901 GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC CCGTACTATT ACGGCACGAG CCACTGGTAT TTCGACGTCT GGGTCAAGG AACCTTGGTC
CGCGGACTC CTGTGACGGC AGATAATGAC AGTTTTCATG GGCATGATAA TGCCGTGCTC GGTGACCATA AAGCTGCAGA CCCCAGTTCC TTGGGACCAG
110 R A E D T A V Y Y C A K Y P Y Y Y G T S H W Y F D V W G Q G T L V
2001 ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCTGTGCCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGC TGCCCTGGTCA
TGGCAGAGGA GCCGGAGGTG GTTCCCGGT AGCCAGAGG GGGACCGTGG GAGGAGGTTT TCGTGGAGAC CCCCCTGTG CCGGACCCG ACGGACCAGT
143 T V S S A S T K G P S V F P L A P S S K S T S G T A A L G C L V K
2101 AGGACTACTT CCCCAGAACG GTGACGGTGT CGTGGAATC AGGGCCCTG ACCAGCGGG TGCACACCTT CCCGGCTGTC CTACAGTCTT CAGGACTCTA
TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA GGGCCGACAG GATGTCAGGA GTCCTGAGAT
177 D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y
2201 CTCCTCAGC AGCGTGGTGA CTGTGCCCTC TAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG
GAGGAGTCG TCGCACCACT GACACGGGAG ATCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTGGGT CGTTGTGGTT CCACCTGTTT
210 S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K
2301 AAAGTTGAGC CCAATCTTG TGACAAAACCT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGG GACCGTCAGT CTTCTCTTC CCCCCAAAAC
TTTCAACTCG GGTTAGAAC ACTGTTTGA GTGTGTACGG GTGGCAGGG TCGTGGACTT GAGGACCCCT CTGGCAGTCA GAAGGAGAAG GGGGTTTTG
243 K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P P K P
2401 CCAAGGACAC CCTCATGATC TCCCGGACCC CTGAGGTGAC ATGGTGGTG GTGGAGCTGA GCCACGAAGA CCTGAGGTG AAGTTCAACT GGTACGTGGA
GGTTCCTGTG GGAGTACTAG AGGGCCTGGG GACTCCAGTG TAGGCACCAC CACTTGCCTT CCGTGTCTT GGGACTCCAG TTCAAGTTGA CCATGCACCT
277 K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V D

FIG. 3C

2501 CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGGGGGAG GAGCAGTACA ACAGCAGCTA CCGTGTGGTC AGCGTCTCTCA CCGTCTCTGCA CCAGGACTGG
GCCGCACCTC CAGGTATTAC GGTTCTGTTT CGGCGCCCTC CTCGTCAATG TGCTGTGCAT GGCACACCAG TCGCAGGAGT GGCAGGACGT GGTCTGTACC
310 G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W

2601 CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAG CCTCCCCAGC CCCCATGGAG AAACCATCT CCAAGGCCAA AGGGCAGCCC CGAGAACCAC
GACTTACCGT TCCTCATGTT CAGGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGTAGCTC TTTTGGTAGA GGTTCGGTT TCCCGTCGG GCTCTTGGTG
343 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q

2701 AGGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACCAA GAACCAGGTC AGCTGACCT GCCTGGTCAA AGGCTTCTAT CCAGCGCACA TCGCCGTGGA
TCCACATGTG GGACGGGGGT AGGGCCCTTC TCTACTGTT TCTGGTCCAG TCGGACTGGA CGGACCAGTT TCCGAAGATA GGTCTGCTGT AGCGGCACCT
377 V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E

2801 GTGGAGAGC AATGGGCAGC CGGAGAACAA CTACAGACC ACGCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCTCT ACAGCAAGCT CACCGTGGAC
CACCTCTCG TTACCCGTCG GCCTCTTGT GATGTTCTGG TCGGAGGGC ACACCTGAG GCTGCCGAGG AAGAAGGAGA TGTGTTTGA GTGGCACCTG
410 W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D

2901 AAGAGCAGGT GGCAGCAGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACCTACA CGCAGAAGAG CTCTTCCCTG TCTCCGGGTA
TTCTCGTCCA CCGTCGTCC CTTGCAGAAG AGTACGAGC ACTACGTA CCGAGACGTG TTGGTATGT GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT
443 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K

3001 AATAAGCATG CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT GTTAACCTCAT GTTGGACAGC TTATCATCGA TAAGCTTTAA
TTATTCTGAC GCTGCCGGGA TCTCAGGGAT TCGGAGCCAA CGGCGGCCCG CAAAAATAA CAATTGAGTA CAACTGTG AATAGTAGCT ATTCGAAATT
477 O

3101 TCGGAGTATT TATCAGAGTT AAATTGCTAA CGCAGTCAGG CACCGTGAT GAAATCTAAC AATGGCTCA TCGTCACTCT CGGCACCGTC ACCCTGGATG
ACGCCATCAA ATAGTGTCAA TTTAAGGATT GCGTCAGTCC GTGGCACATA CTTTAGATTG TTACGGAGT AGCAGTAGGA CCCGTGGCAG TGGGACCTAC
^Start Tet Resistance Coding Sequence

3201 CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGGGGAT ATCGTCCATT CCGACAGCAT CGCCAGTCA TATGGCGTGC TGCTAGCGCT
GACATCCGTA TCCGAACCAA TAGGGCCATG ACGGCCCGGA GAACGCCCTA TAGCAGGTAA GGCTCTGTA GCGTCTAGT ATACCGCAGC ACGATCGCGA

FIG. 3D

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1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAGAAGA AGAGTCGAAT
  CTTAAGTTGA AGAGGTATGA AACCTATTCC TTATATGCTG TACTTTTTAG AGTAAAGCACT CAACAATAAA TTCSAACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACTGTGTG GCGAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
  CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTTAC TGGTGTGCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCACTA
  CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCTATA AGTTGTCACG GCGGAGACTT ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTGTAACTA GTACGGCAAGT
  TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTCTCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC
  AGTGCATTTT TCCCATAGAT CTTAATACCT CTTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTGGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I ^Light chain
  ^STII signal TIR -1

501 CAGTTGACCC AGTCCCGGAG CTCCCTGTCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGCGCAA GTCAGGATAT TAGCAACTAT TTAAGTGGT
  GTCAACTGGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG AGTCTCGGTT CAGTCTCTATA ATCGTTGATA AATTGACCA

26 Q L T Q S P S S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGGAAAA GCTCCGAAAG TACTGATTTA CTTACCTCC CTCTCTCCACT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
  TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G T

701 GGATTTCACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTGCGAACTT ATTACTGTCA ACAGTATAGC ACCGTGCCGT GGACGTTTGG ACAGGGTACC
  CCTAAAGTGA GACTGGTAGT CGTCAGACGT CCGTCTTCTG AAGCGTTGAA TAATGACAGT TGTCATATCG TGGCAGCGCA CTGCAAAACC TGTCCTCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGGAGA TCAAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
  TTCCACCTCT AGTTGTGCTTG ACACCGAGGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA CACACGGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

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FIG. 4A

901 TGAATAACTT CTATCCAGA GAGGCCAAG TACAGTGGAA GGTGATAAC GCCCTCCAAT CCGGTAATC CCAGGAGAGT GTCACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTACACCTT CCACCTATTG CCGGAGGTTA GCCCATTTAG GGTCTCTTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K
1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
CCTGTCGTGG ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGCTGA TGCTCTTGT GTTTCAGATG CCGACGCTTC AGTGGTAGT CCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGA GAGTGTAAAT TAAATCCTCT ACGCCGGAGC CATCGTGGC AGCTCGGTAC CCGGGATCT AGGCCTAACG
AGCGGGCAGT GTTCTCGAA GTTGTCCTTCT CTCACAATTA ATTAGGAGA TCGCGCCTGC GTAGCACCGC TCGAGCCATG GGCCCTAGA TCCGGATTGC
226 S P V T K S F N R G E C O
lambda to terminator
1201 CTCGGTTGCC GCCGGCGTT TTTTATTGTT GCCGACGCG ATCTCGAATG AACTGTGTGC GCAGGTAGAA GCTTTGGAGA TTATCGTCAC TGCAATGCTT
GAGCCACGG CCGCCCGCAA AAAATAACAA CGGCTGCGG TAGAGCTTAC TTGACACACG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA
1301 CGCAATATGG CGCAAAATGA CCAACAGCG TTGATTGATC AGGTAGAGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCTGAC GACGATACGG
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCCATCTCCC CCGGACATG CTCATTTCG GGTACGGTC GTAAGGACTG CTGCTATGCC
1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACGG CCGAGACTTA
TCGACGACGC GCTAATGCAT TTCTTCAATA ACTTCGTAGG AGCAGTCATT TTCAATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGCTCTGAAT
1501 TAGTCGCTTT GTTTTATTT TTTAATGTAT TTGTAAGTAT TACGCAAGTT CACGTAAAAA GGGTATCTAG AATTATGAAG AAGAATATCG CATTCTTCT
ATCAGCGAAA CAAAAATAAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCGATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA
1
M K K N I A F L L
^STII Signal TIR-1
1601 TGCATCTATG TTCGTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTC AGCTGGTGA GTCTGGCGT GGCCTGGTGC AGCAGGGGG CTCACCTCGT
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGGCGATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC GAGTGAGGCA
10 A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R
^start heavy chain

FIG. 4B

1701 TTGTCCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG GTATAAAGTGGTCCGTCAG GCGCCGGGTA AGGCCCTGGA ATGGGTTGGA TGGATTAAACA
AACAGGACAC GTCGAAGACC GATATGAAG TGGTTGATAC CATATTGAC CCAGGCAGTC CCGGGCCCAT TCCCGGACCT TACCCAACCT ACCTAATTGT
43 L S C A A S G Y T F T N Y G I N W V R Q A P G K G L E W V G W I N T

1801 CCTATACCGG TGAACCGACC TATGCTGGG ATTTCAAAG TCGTTTCACT TTTTCTTAG ACACCTCCA AAGCACAGCA TACCTGCAGA TGAACAGCCT
GGATATGGCC ACTTGCTGG ATACGACGCC TAAAGTTGAC AGCAAAGTGA AAAAGAAATC TGTGGAGGT TTCGTGTCGT ATGGACGTCT ACTTGTCGGA
77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L

1901 GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC CCGCACTATT ATGTGAACGA GCGGAAGAGC CACTGGTATT TCGACGTCTG GGGTCAAGGA
CGCGCGACTC CTGTGACGGC AGATAATGAC ACGTTTCAATG GCGGTGATAA TACACTTGCT CGCCTTCTCG GTGACCAATAA AGCTGCAGAC CCCAGTTCTT
110 R A E D T A V Y Y C A K Y P H Y Y V N E R K S H W Y F D V W G Q G

2001 ACCCTGGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC CCGTCCCAAG GCACCTCTGG GGGCACAGCG GCCCTGGGCT
TGGGACCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGGG GGACCGTGGG AGGAGTTCT CGTGGAGACC CCGTGTGCG CCGGACCCGA
143 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C

2101 GCCTGGTCAA GGACTACTTC CCGGAACCGG TGACGGGTGC GTGGAATCA GCGCCCTGGA CCAGCGGGGT GCACACCTTC CCGGTGTTC TACAGTCTTC
CGGACCAGTT CCTGATGAAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTGCGCGCA CGTGTGGAAG GCGCGACAGG ATGTCAGGAG
177 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S

2201 AGGACTCTAC TCCTCAGCA GCGTGGTGAC TGTGCCCTCT AGCAGTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCAG CAACACCAAG
TCCTGAGATG AGGGAGTCGT CGACCACTG ACACGGGAGA TCGTGAAC TCGTGGTCTG GATGTAGAGG TTGCACCTAG TGTTCGGGTC GTTGTGGTTC
210 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K

2301 GTGGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGG ACCGTGATC TTCCTCTTCC
CACCTGTTCT TTCAACTCGG GTTTAGAACA CTGTTTGGAG TGTGTACGGG TGGACGGGT CGTGGACTTG AGGACCCCCC TGGCAGTCAG AAGGAGAAGG
243 V D K K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P

2401 CCCCCAAACC CAAGGACACC CTCATGATCT CCGGACCCC TGAGGTCA TCGTGTGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG
GGGGTTTTGG GTTCCTGTGG GAGTACTAGA GGGCCCTGGG ACTCCAGTGT ACGCACACC ACCTGCATC GGTGCTTCTG GGACTCCAGT TCAAGTTGAC
277 P K P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W

FIG. 4C

2501 GTACGTGGAC GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCAGGTAC CGTGTGGTCA GCGTCTCTAC CGTCTCTGCAC
CATGCACCTG CCGCACCTCC AGTATTACG GTTCTGTTTC GCGCCCTCC TCGTCATGTT GTCGTGCATG GCACACCAGT CGCAGGAGTG GCAGGACGTG
310 Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H

2601 CAGGACTGGC TGAATGGCAA GGAGTACAAG TGCAAGGTCT CCAACAAAGC CCTCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA GGGCAGCCCC
GTCCTGACCG ACTTACCGTT CCTCATGTTT ACCTTCCAGA GGTGTTTCG GGAGGTTCG GGGTAGCTCT TTTGGTAGAG GTTTCGGTTT CCGTCGGGG
343 Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R

2701 GAGAACCAACA GGTGTACACC CTGCCCCCAT CCGGGGAAGA GATGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT
CTCTTGGTGT CCACATGTGG GACGGGGTA GGGCCCTTCT CTACTGGTTC TTGGTCCAGT CGGACTGGAC GGACCAGTTT CCGAAGATAG GGTGCGTGTGTA
377 E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I

2801 CCGCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCTCTA CAGCAAGCTC
GGGGCACCTC ACCCTCTCGT TACCCGTCGG CCTCTTGTG ATGTTCTGGT GCGGAGGGA CGACCTGAGG CTGCCGAGGA AGAAGGAGAT GTCGTTCCGAG
410 A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L

2901 ACCGTGGACA AGAGCAGGTG GCAGCAGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT
TGGCACCTGT TCTCGTCCAC CGTCGTCCCC TTGCAGAAGA GTACGAGGCA CTACGTACTC CGAGACGTGT TGGTGATGTG CGTCTTCTCG GAGAGGGACA
443 T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S

3001 CTCGGGGTAA ATAGCATGC GACGGGCCCTA GAGTCCCTAA CGCTCGGTG CCGCCGGGG TTTTATTG TTAACATG TTTGACAGCT TATCATCGAT
GAGGCCATT TATTCTACG CTGCCGGGAT CTCAGGGATT GCGAGCCCAAC GCGGCCCGC AAAAAATAAC AATTGAGTAC AAAGTGTGCA ATAGTAGCTA
477 P G K O

^lambda terminator

3101 AAGCTTTAAT GCGGTAGTTT ATCACAGTTA AATTGCTAAC GCAGTCAGC ACCGTGTATG AAATCTAACA ATGGCTCAT CGTCATCCTC GGCACCGTCA
TTGGAATTA CGCCATCAA TAGTGTCAT TTAACGATTG CGTCAGTCCG TGGCACATAC TTTAGATTGT TACGCGAGTA GCAGTAGGAG CCGTGGCAGT

3201 CCTGGATGC TGTAGCATA GGCTTGGTTA TGCCGGTACT GCCGGGCCCTC TTGCG
GGGACCTAG ACATCGGTAT CCGAACCAAT ACGGCCATGA CCGCCCGGAG AACGC

FIG. 4D

1 ATCGATGAAT TCATGCTGTG GTGTCAATGTT CCGTGATCGC CAGGGTGCCG ACGGCATCTT CGACTGCAGG GTGCACCAAT GCTTCTGGCG TCAGGCAGCC
TAGCTACTTA AGTACGACAC CACAGTACCA GCCACTAGCG GTCCACCGC TCGCGGTAGA GCTGACGTGC CACGTGGTTA CGAAGACCGC AGTCCGTGGG
^ClaI

101 ATCGAAGCT GTGGTATGGC TGTGCAGGTC GTAAATCACT GCATAATTCG TGTGCTCAA GGGGCATCC CGTCTCGAT AATGTTTTT GCGCCGACAT
TAGCCTTGA CACCATACCG ACACGTCCAG CATTTAGTA CGTATTAGC ACAGCGAGTT CCGCGTGAGG GCAAGACCTA TTACAAAAA CCGCGCTGTA

201 CATAACGGTT CTGGCAAATA TTCTGAAATG AGCTGTTGAC AATTAATCAT CGAATAGTT TAATGTGGG AATTGTGAGC GGATAACAAT TAAGCTTAGG
GTAATGCCAA GACCGTTTAT AAGACTTTAC TCGACAACTG TTAATTAGTA GCTTGATCAA ATTACACACC TTAACACTCG CCTATTGTTA ATTGGAATCC

301 ATTCTAGAGG GAAGATTTAT GAAATCACTG TTAAAGTAA CGCTGCTGGC GACCACAATG GCCGTTGCC TGCATGCACC AATCACTTTT GCTGCTGAAG
TAAGATCTCC CTTCTAAATA CTTTAGTGAC AATTTCAAT GCGACGACCG CTGGTGTTAC CGGCAAGGG ACGTACGTGG TTAGTGAAAA CGACGACTTC
M K S L F K V T L L A T T M A V A L H A P I T F A A E A
^fkpA start

401 CTCGAAAACC TGCTACAGCT GCTGACAGCA AAGCAGGTT CAAAATGAC GATCAGAAAT CAGCTTATGC ACTGGTGCC TCGCTGGGTC GTTACATGGA
GACGTTTTGG ACGATGTCGA CGACTGTCGT TTGTCGCAA GTTTTACTG CTAGTCTTA GTCGAATACG TGACCCACGG AGCGACCCAG CAATGTACCT
29 A K P A T A A D S K A A F K N D D Q K S A Y A L G A S L G R Y M E

501 AAACCTCTCTA AAAGAACAAG AAAAAGTGG CATCAAACTG GATAAAGATC AGCTGATCGC TGGTGTTCAG GATGATTTG CTGATAAGAG CAAACTCTCC
TTTGAGAGAT TTCTTTGTTT TTTTGGACCC GTAGTTTGAC CTATTTCTAG TCGACTAGCG ACCACAAGTC CTACGTAAAC GACTATTCTC GTTTGAGAGG
62 N S L K E Q E K L G I K L D K D Q L I A G V Q D A F A D K S K L S

601 GACCAAGAGA TCGAACAGAC TCTACAAGCA TTGCAAGCTC GCGTGAAGTC TTCTGCTCAG GCGAAGATGG AAAAAGACGC GGCTGATAAC GAAGCAAAAG
CTGGTTCTCT AGCTTGCTG AGATGTTCTG AAGCTTCGAG CGCACTTCAG AAGACGAGTC CGCTTCTACC TTTTCTGCG CCGACTATTG CTTCTGTTTC
95 D Q E I E Q T L Q A F E A R V K S S A Q A K M E K D A A D N E A K G

701 GTAAAGAGTA CCGCGAGAAA TTTCGCAAG AGAAGGTTGT GAAACCTCT TCAACTGGTC TGGTTTATCA GGTAGTAGAA GCCGGTAAAG GCGAAGCACC
CATTTCTCAT GCGCTCTTTT AAACGGTTTC TCCTTCCACA CTTTGGAGA AGTTGACCAG ACCAAATAGT CCATCATCTT CCGCATTTTC CGCTTCGTGG
129 K E Y R E K F A K E K G V K T S S T G L V Y Q V V E A G K G E A P

FIG. 5A

801 GAAAGACAGC GATACTGTTG TAGTGAAC TA TAGTACGACG GTAAAGAGTT CGACAAC TCT TACACCCG TG GTGAACCGCT TTCTTTCCGT
CTTTCTGTG CTATGACAC ATCACTTGAT GTTTCATGC GACTAGCTGC CATTTCTCAA GCTGTTGAGA ATGTGGGCAC CACTTGGCGA AAGAAAGGCA
162 K D S D T V V V N Y K G T L I D G K E F D N S Y T R G E P L S F R
901 CTGGACGGTG TTATCCCGGG TTGGACAGAA GGTCTGAAGA ACATCAAGAA AGCGGTAAG ATCAAACTGG TTATTCCACC AGAAGTGGCT TAGCGCAAAG
GACCTGCCAC AATAGGGGCC AACCTGTCTT CCAGACTTCT TGTAGTTCTT TCCGCCATTG TAGTTTGACC AATAAGGTGG TCTTGACCGA ATGCCGTTTC
195 L D G V I P G I P G W T E G L K N I K K I K L V I P P E L A Y G K A
1001 CGGGTGTTC GGGATCCCA CCGAATTCTA CCCTGGTGTG TGACGTAGAG CTGCTGGATG TGAACCCAGC GCCGAAGGCT GATGCAAAGC CGGAAGCTGA
GCCCCAAGG CCCCTAGGGT GGCTTAAGAT GGGACCACAA ACTGCATCTC GACGACCTAC ACTTTGGTGG CGGCTTCCGA CTACGTTTCG GCCTTCGACT
229 G V P G I P P N S T L V F D V E L L D V K P A P K A D A K P E A D
1101 TCGGAAGCC GCAGATTCTG CTAAAAATA AAAGCTAGC
ACGCTTTCGG CGTCTAAGAC GATTTTAT TTTGATCG
262 A K A A D S A K K O
^NheI

FIG. 5B

1 GAATTCAACT TCTCCAFAC TGGATAAGG AATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCIG TACTTTTITAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTCTCT TCTCAGCTTA
^EcoRI

101 GAACCTGTGT CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTGCG CAACCTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCCTGA CGACGATPAC GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACCTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACA GCTGTCTATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTTGTAAC TA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGTATCTA GAATTATGAA AAAGAATATC GCATTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGTA CGCTGATATC
AGTGCAATTT TCCCATAGAT CTTAATACTT TTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTCGCGAT CGGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^start STII signal TIR 7 anti-TF light chain^

501 CAGATGACCC AGTCCCGGAG CTCCTGTGTC GCGATAGGGT CACCATCACC TGCAGAGCCA GTCCGACAT CAAGAGCTAT CTGAACCTGGT
GTCTACTGGG TCAGGGGCTC GAGGACAGG CGGACACACC CGCTATCCCA GTGTAGTGG ACGTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTGCTG AAGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC
TAGTTGCTTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GATAGGATGA TCAGAGCGAC TTCTCAGGG AAGAGCGAAG AGACTAGGC CAAGACCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTGCAACTT ATTACTGTCT TCAGCAGGA GAGTCTCCAT GGACATTGG ACAGGATACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGGTTTGA TAATGACAGA AGTCTGCTCT CTGAGAGGA CTTGTAAACC TGTCCCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

FIG. 6A

801 AAGGTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCATCTGAT GAGCAGTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTAGACCTTG AGAAGACAA CACACGGACG
126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CCGGTAACTC CCAGGAGAGT GTCACAGAGC AGACAGACAA
ACTTATTGAA GATAGGGTCT CTCGGGTTTC ATGTACCTT CCACCTATTG CCGGAGGTTA GCCCTCTCA CAGTGTCTCG TCCTGTCTGTT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA GCAGCACCTT GAGGCTGAGC AAAGCAGACT AGAGAAACA CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTGGAGT CCGTCTGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG CCGACGCTC AGTGGGTAGT CCCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAT TAAATCCTCT AGCCCGGACG CATCGTGGCG AGCTCGGTAC CCGGGGATCT AGGCCTAAGC
AGCGGGCAGT GTTCTCTGAA GTTGTCCCT CTCACAAATTA ATTAGGAGA TCGGGCCTGC GTAGCACCGC TCGAGCCATG GGGCCCTAGA TCGGGATTGC
226 S P V T K S F N R G E C O

lambda t0 terminator^

1201 CTCGGTTGCC GCCGGCGGTT TTTTATTGTT GCCGACGGC ATCTCGACTG CACGGTGAC CAATGCTTCT GCGGTCAGG AGCATCGGA AGCTGTGGTA
GAGCCAACGG CCGCCCGCAA AAAATNACAA CCGCTGCGCG TAGAGCTGAC GTGCCACGTG GTTACGAAGA CCGCAGTCCG TCGGTAGCCT TCGACACCAT

1301 TGGCTGTGCA GGTCTGTAAT CACTGCATAA TTCGTGTGCG TCAAGGGCA CTCGCCGTTCT GGATAATGTT TTTTGGCGCG ACATCATAC GGTCTCTGGCA
ACCGACACGT CCAGCATTTA GTGACGTATT AAGCACAGCG AGTTCGCGGT GAGGGCAAGA CCTATTACAA AAAACGGCGC TGTAGTATTG CCAAGACCGT

1401 AATATTCTGA AATGAGCTGT TGACAATTAA TCATCGAACT AGTTTAAATGT GTGGAATTGT GAGCGGATAA CAATTAAAGT TAGGATCTAG AATTATGAAG
TTATAAGACT TTAATCGACA ACTGTTAATT AGTAGCTTGA TCAAAATTACA CACCTTAACA CTCGCCATT GTTAATTGA ATCTAGATC TTAATACTTC

1 M K
Start STII signal TIR 3^

1501 AAGAAATATTG CGTTCCTACT TGCTCTATG TTGTCTTTT CTATAGCTAC AAACGGTAC GCTGAGTTC AGCTGTGGA GTCTGGCGGT GGCCTGGTGC
TTCTTATAAC GCAAGGATGA ACGGAGATAC AAACAGAAAA GATATCGATG TTTGGCGATG CGACTCCAG TCGACCACT CAGACCGCCA CCGGACCAAG
3 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V Q

^anti-TF heavy chain

FIG. 6B

1601 AGCCAGGGG CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTTCAATATT AAGAGTACT ACATGCACTG GGTCCGTCAG GCCCGGGTA AGGGCCTGGA
TCGGTCCCC GAGTGAGGCA AACAGGACAC GTGGAAGACC GAAGTTATAA TTCTCATGA TGTACGTGAC CCAGGCAGTC CGGGGCCCAT TCCCGACCT
37 P G G S L R L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E

1701 ATGGTTGA TTGATTGATC CAGAGCAAGG CAACAGATC TATGACCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA
TACCCAAACCT AACTAACTAG GTCTCGTTCC GTTGTGCTAG ATACTGGGCT TCAAGGTCCT GGCACGGTGA TATTCGGAC TGTAAAGTT TTTGTGTCTG
70 W V G L I D P E Q G N T I Y D P K F Q D R A T I S A D N S K N T A

1801 TACCTGCAGA TGAACAGCCT GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTGAGAC ACGGCGCTT ACTTCGACTA CTGGGTCAA GGAACCTGG
ATGGACGTCT ACTTGTCGGA CGCAGCACTC CTGTGACGGC AGATAATAAC ACAGCTCTG TCGCGGGCAA TGAAGCTGAT GACCCAGTT CTTGGGACC
103 Y L Q M N S L R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V

1901 TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT CCCCCTGGCA CCCTCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GGTGCCTGGT
AGTGGCAGAG GAGCCGAGG TGGTTCCCG GTAGCCAGAA GGGGACCGT GAGGAGGAGT TCTGTGGAG ACCCCCGTGT CGCCGGGACC CGACGGACCA
137 T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L V
^ApaI

2001 CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGAAC TCAGGCGCC TGACCAGCG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
GTTCTGATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGG ACTGGTCGCC GCACGTGTGG AAGGGCCGAC AGGATGTGAG GAGTCCTGAG
170 K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L

2101 TACTCCCTCA GCAGCGTGGT GACTGTGCC TCTAGCAGT TGGGCACCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA
ATGAGGGAGT CGTCGCACCA CTGACACGGG AGATCGTGA ACCCGTGGT CTGGATGTAG ACGTGCACT TAGTGTCCG GTCGTTGTTG TTCCACCTGT
203 Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K

2201 AGAAAGTTGA GCCCAAATCT TGTGACAAA CTCACACATG CCCACCGTC CCAGCACCTG AACTCCTGG GGGACCGTCA GTCTTCTCT TCCCCCAA
TCTTCAACT CGGGTTTGA AACTGTTT GAGTGTGTAC GGGTGGCAG GGTGCTGGAC TTGAGGACCC CCCTGGCAGT CAGAAGGAGA AGGGGGTTT
237 K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P P K

FIG. 6C

2301 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGGCGTG TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG
TGGGTTCTTG TGGGAGTACT AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGTCT CTGGGACTCC AGTTCAAGTT GACCATGCAC
270 P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V
2401 GACGCGCTGG AGGTGCATAA TGCCAAAGCA AAGCGCGCGG AGGAGCAGTA CAACAGCAGG TACCGTGTGG TCAGCGTCTCT CACCGTCTCTG CACCAGGACT
CTGCGGCACC TCCACGTATT ACGGTTCTGT TTGCGCGGCC TCCTCGTCAT GTTGTCGTGC ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCTCTGA
303 D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W
2501 GGCTGAATGG CAAGGAGTAC AAGTGCAGG TCTCCAAACA AGCCCTCCCA GCCCCCATCG AGAAACCAT CTCCAAAGCC AAAGGCGAGC CCCGAGAAAC
CCGACTTACC GTTCCTCATG TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTGGTA GAGGTTCTGG TTTCGCGTGG GGGCTCTTGG
337 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P
2601 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA AGAGATGACC AAGAACCAGG TCAGCCTGAC CTGCTGTGTC AAAGCTTCT ATCCAGCGA CATCGCGGTG
TGTCCACATG TGGACGGGG GTAGGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGACTG GACGACCAG TTTCGGAAGA TAGGTCGCT GTAGCGGCAC
370 Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V
2701 GAGTGGGAGA GCAATGGGCA GCGGAGAAC AACTACAAGA CCACGCTCC CGTGTGGAC TCCGAGGCT CTTCTTCTCT CTACAGCAAG CTCACGCTGG
CTCACCTCT CGTTACCGT CGGCTCTCTG TTGATGTTCT GTGCGGAGG GCACGACTG AGGCTGCCGA GGAAGAAGGA GATGCTGTC GAGTGGCACC
403 E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D
2801 ACAAGAGCAG GTGGCAGCAG GGGACGTCT TCTCATGCTC CGTGATGCT GAGGCTCTGC ACAACCACTA CAGCAGAGG AGGCTCTCCC TGTCCTCCGG
TGTTCTCGTC CACCGTCGTC CCCTTGCGA AGAGTACGAG GCACTACGTA CTCGAGACG GTTGTGTGAT GTGCTCTTC TCGGAGAGGG ACAGAGGCC
437 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G
2901 TAAATAAGCA TGGACGGCC CTAGAGTCCC TAACGCTCGG TTGCGCGCGG GCGTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT
ATTATTCTGT ACCGTGCGG GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAT AACAACTGT TACAACACTGT CGAATAGTAG CTATTGGA
470 K O

FIG. 6D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTATGTCTG TACTTTTATG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG GCGAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GGGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CCGGTTTTAC TGGTTGTCCG CAACTAACTA GTCCATCTCC

201 GGGCGCTGPA CGAGGTAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTGAGTA
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCAACA GCTGTCAATA AGTTGTCACG GCCGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAATGTA TTTGTAACTA GTACGCAAGT
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CCGCTCTGAA TATCAGCGAA ACAAAATAA AAANTTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGGTATCTA GAATTATGAA AAAGAAATATC GCATTTCCTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGCTA CGCTGATATC
AGTGCATTTT TCCCATAGAT CTTAATACTT TTCTTTATAG CGTAAAGAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTTGCGCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I
^Start STII signal TIR 7 anti-tissue factor light chain^

501 CAGATGACCC AGTCCCGGAG CTCCTGTGCC GCCTGTGG GCGATAGGT CACCATACC TGCAGAGCCA GTCCGACAT CAAGAGCTAT CTGAACCTGGT
GTCTACTGG TCAGGGGCTC GAGGGACAGG CCGATATCCA GTGCTAGTG AGTCTCTGGT CAGCGTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTA CTATGTACT AGTCTCGCTG AAGGAGTCCC TTCTCGCTC TCTGGATCCG GTTCTGGGAC
TAGTTGTCTT TGGTCTTTT CGAGGCTTTC ATGACTAAAT GATACATGA TCAGAGCGAC TTCCTCAGG AGAGCGAAG AGACCTAGGC CAAGACCCCTG

60 Q Q K P G K A P K V L I Y Y A T S L A E G V P S R F S G S G T

701 GGATTACACT CTGACCATCA GCAGTCTGCA GCCAGAGAC TTCCGAACTT ATTACTGTCT TCAGCAGCGA GAGTCTCCAT GGACATTGG ACAGGGTACC
CCTAATGTGA GACTGGTAGT CGTCAGACGT CCGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCTGCTCT CTCAGAGGTA CCTGTAAACC TGTCCTCATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGGAGA TCAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC
TTCCACCTCT AGTTTGCTTG ACACCGACGT GGTAGACAGA AGTAGAAGGG CCGTAGACTA CTCGTCAACT TTACACCTTG ACGAAGACAA CACACGGAGC

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

FIG. 7A

901 TGAATAACTT CTATCCCGA GAGGCCAAG TACAGTGGAA GGTGGATAAC GGCCTCCAAT CGGTAACATC CCAGGAGAGT GTACAGAGC AGGACAGCAA
ACTTATTGAA GATAGGGTCT CTCGGGTTT ATGTACCTT ATGTACCTT GCGAGGTTA GCCCATTTAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT
160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K
1001 GGACAGCACC TACAGCCTCA GACGACCCCT GACGCTGAGC AAAGCAGACT ACAGAGAAACA CAAAGTCTAC GCTGGGAAG TCACCCATCA GGGCCTGAGC
CCTGTCTGG ATGTCTGGAGT CGTCTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTCAGATG CCGACGCTTC AGTGGGTAGT CCGGACTCG
193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S
1101 TCGCCCGTCA CAAAGAGCTT CAAAGGGGA GAGTGTAAAT TAAATCCTCT AGCCCGGAGC CATCGTGGCG AGCTCGGTAC CCGGGATCT AGGCTAAGC
AGCGGGCAGT GTTCTCGAA GTTGTCCCT CTCACAATTA ATTAGGAGA TCGGGCCTGC GTAGCACCGC TCGAGCCATG GGGCCCTAGA TCGGATTCG
226 S P V T K S F N R G E C O
lambda t0 terminator^
1201 CTCGGTTGCC GCCGGGCGT TTTTATTGTT GCGGACGCG ATCTCGACTG CACGGTGAC CAATGCTTCT GCGTCAAGC AGCCATCGGA AGCTGTGGTA
GAGCCAACGG CGGCCCGCAA AAAATAACAA CCGCTGCGG TAGAGCTGAC GTGCCACGTG GTTACGAAGA CCGCAGTCCG TCGTAGCCT TCGACACCAT
1301 TGGCTGTGCA GGTGTAAT CACTGCATAA TTCGTGTGCG TCAAGGGCA CTCGCCGTTCT GGATAATGTT TTTTGGCGG ACATCATAC GGTCTCTGGCA
ACCGACACGT CCAGCATTA GTGACGTAAT AAGCACAGCG AGTCCGCGT GAGGGCAAGA CCTATTACAA AAAACGCGG TGTAGTATTG CCAAGACCGT
1401 AATATTCTGA AATGAGCTGT TGACAATTAA TCATCGAAT AGTTTAATGT GTGGAATGT GAGCGGATAA CAATTAAGCT TAGGATCTAG AATTATGAAG
TTATAAGACT TTAATCGACA ACTGTTAAT AGTAGCTTGA TCAATTAACA CACCTTAACA CTCGCCATTT GTTAATTGA ATCTAGATC TTAATATCTC
1
M K
Start STII signal TIR 3^
1501 AAGAAATATTG CGTTCCTACT TGCCTCTATG TTTGTCTTTT CTATAGCTAC AAACGCGTAC GCTGAGGTTT AGCTGGTGA GTCTGGCGGT GGCCTGGTC
TTCTTATAAC GCAAGGATGA ACGGAGATAC AACAGAGAAA GATATCGATG TTTGGCGATG CGACTCCAAG TCGACCACTT CAGACCGCCA CCGGACCACG
3 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V Q
anti-tissue factor heavy chain with cys to ser in hinge^
1601 AGCCAGGGGG CTCACTCCGT TTGTCTCTGG CAGCTTCTGG CTTCATATT AAGGAGTACT ACATGCACTG GGTCCGTGAG GCCCGGGTA AGGCTCTGGA
TCGGTCCCCC GAGTGAGCA AACAGGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCACTC CCGGGCCCAT TCCCGGACCT
37 P G G S L R L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E

FIG. 7B

1701 ATGGGTTGGA TTGATTGATC CAGAGCAAGG CAACACGATC TATGACCGA AGTTCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCCAA AAACACAGCA
TACCAACCT AACTAACTAG GTCTCGTTCC GTTGCTGCTAG ATACTGGGCT TCAAGGTCTT GGCACGGTGA TATTCGGAC TGTTAAGTT TTTGTGTCGT
70 W V G L I D P E Q G N T I Y D P K F Q D R A T I S A D N S K N T A

1801 TACCTGCAGA TGAACAGCCT GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCGCTT ACTTCGACTA CTGGGTCAA GGAACCCCTGG
ATGGACGTCT ACTTGTCGGA CGCAGCACTC CTGTGACGGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCAGTT CTTTGGGACC
103 Y L Q M N S L R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V

1901 TCACCGTCTC CTGGGCTCC ACCAAGGCC CATGGTCTT CCCCTGGCA CCTCTCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG GCTGCCTGGT
AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGACCGT GAGAGGAGGT TCTGCTGGAG ACCCCGCTGT CGCGGGGACC CGACGGACCA
137 T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L V

2001 CAAGGACTAC TTCCCGGAAC CCGTGACGGT GTGCTGGAAC TCAGGGGCC TCAGCAGCG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
GTTCTGATG AAGGGCTTG GCCACTGCCA CAGCACTTG AGTCCGGGG ACTGGTCGCC GCAGCTGTGG AAGGGCCGAC AGGATGTGAG GAGTCTGAG
170 K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L

2101 TACTCCCTCA GCAGCGTGGT GACTGTGCC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCAACAGCC CAGCAACACC AAGTGGACA
ATGAGGGAGT CGTGCACCA CTGACACGG AGATCGTGA ACCCGTGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTTG TTCCACCTGT
203 Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K

2201 AGAAAGTTGA GCCCAAATCT TGTGACAAA CTCACACTAG TCCACCGTCT CCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCTCT TCCCCCAA
TCTTTCACT CGGGTTTGA AACTGTTT GAGTGTGATC AGGTGGCAGA GGTGCTGGAC TTGAGGACCC CCTGGCAGT CAGAAGGAGA AGGGGGGTTT
237 K V E P K S C D K T H T S P P S P A P E L L G G P S V F L F P P K
^Hinge cys to ser ^Hinge cys to ser

2301 ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG TGGTGGACGT GAGCCACGAA GACCTGAGG TCAAGTTCAA CTGGTACGTG
TGGGTTCTCTG TGGGAGTACT AGAGGGCCTG GGGACTCCAG TGTACGCACC ACCACCTGCA CTCGGTGCCT CTGGGACTCC AGTTCAAGTT GACCATGCAC
270 P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V

FIG. 7C

2401 GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGGCGG AGGAGCAGTA CAACAGCAGG TACCGTGTGG TCAGCGTCTT CACCGTCTCG CACCAGGACT
CTGCCGCACC TCCACGATTT ACGGTTCTCT TTCCGGCGCC TCCTCGTCAT GTTGTCGTCG ATGGCACACC AGTCGCAGGA GTGGCAGGAC GTGGTCTCTGA
303 D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W

2501 GGCTGAATGG CAAGGAGTAC AAGTGCAGG TCTCCACAAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAGACC AAAGGGCAGC CCCGAGAACC
CCGACTTACC GTTCTCTCATG TTCACGTTCC AGAGGTTGTT TCGGGAGGGT CCGGGGTAGC TCTTTTGTA GAGGTTTCGG TTTCCTCGTC GGGCTCTTGG
337 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P

2601 ACAGGTGTAC ACCCTGCCCC CATCCCGGGA AGAGATGACC AAGAACGAGG TCAGCCTGAC CTGCCTGGTC AAAGGTTCT ATCCACGGA CATCGCCGTC
TGTCACATG TGGACGGGG GTAGGCCCT TCTCTACTGG TTCTTGGTCC AGTCGACTG GACGGACCAG TTTCGGAAGA TAGGTGCTGT GTAGCGGCAC
370 Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V

2701 GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCAGCGCTCC CGTGTGGAC TCCGAGGGCT CCTTCTTCT CTACAGCAAG CTCACCGTGG
CTCACCTCT CGTTACCCGT CGGCCTCTTG TTGATGTTCT GGTGGGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCGTTT GAGTGGCACC
403 E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D

2801 ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTATGCTC GAGGCTCTGC ACAACCACTA CACGAGAAG AGCTCTCCC TGCTCCGGG
TGTTCTCGTC CACCGTCGTC CCCTTGCAGA AGAGTACGAG GCACTACGTA CTCGAGACG TGTTGGTGAT GTGGTCTTTC TCGGAGAGGG ACAGAGGCCC
437 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G

2901 TAAATAAGCA TGGACGGCC CTAGAGTCCC TAAGCTCGG TTGCGCGCGG GCGTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT
ATTTATTCTG ACGCTGCCGG GATCTCAGG ATTGCGAGCC AACGGCGGCC CGCAAAAAAT AACAACTGT TACAATGAG TACAATGAG CTATTGAAA
470 K O

FIG. 7D

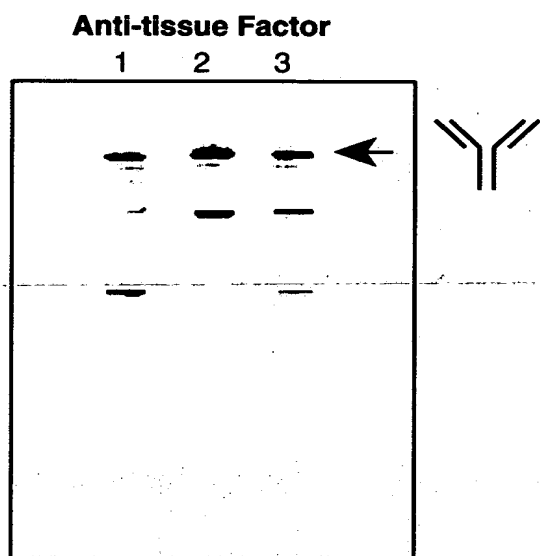


FIG. 8A

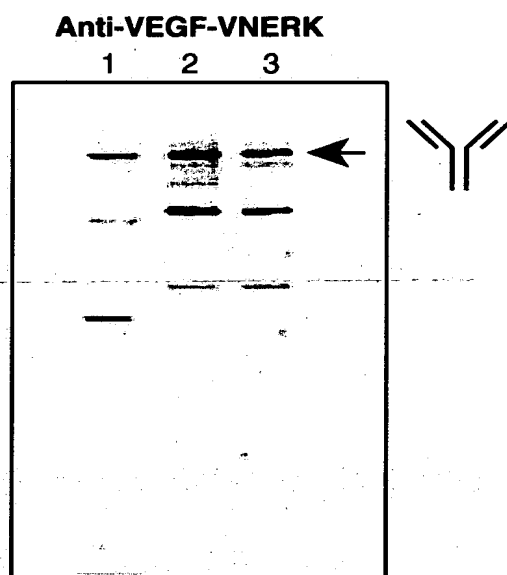


FIG. 8B

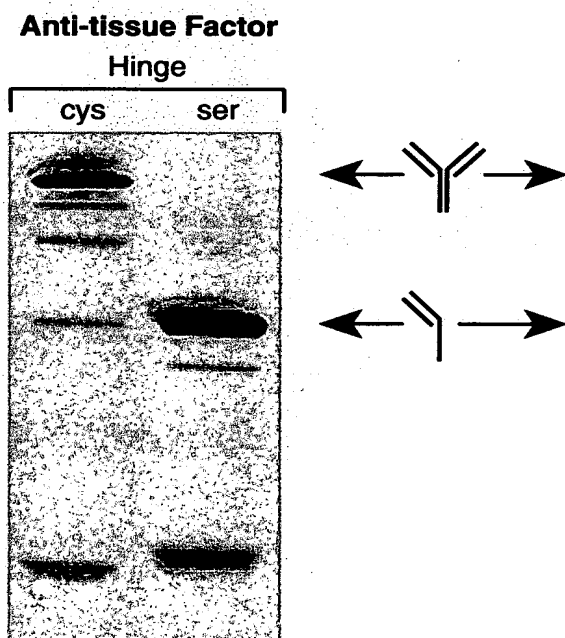


FIG. 9A

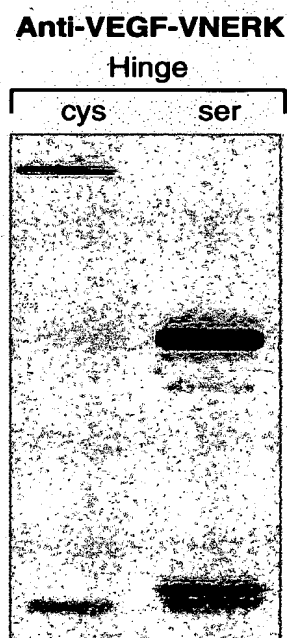
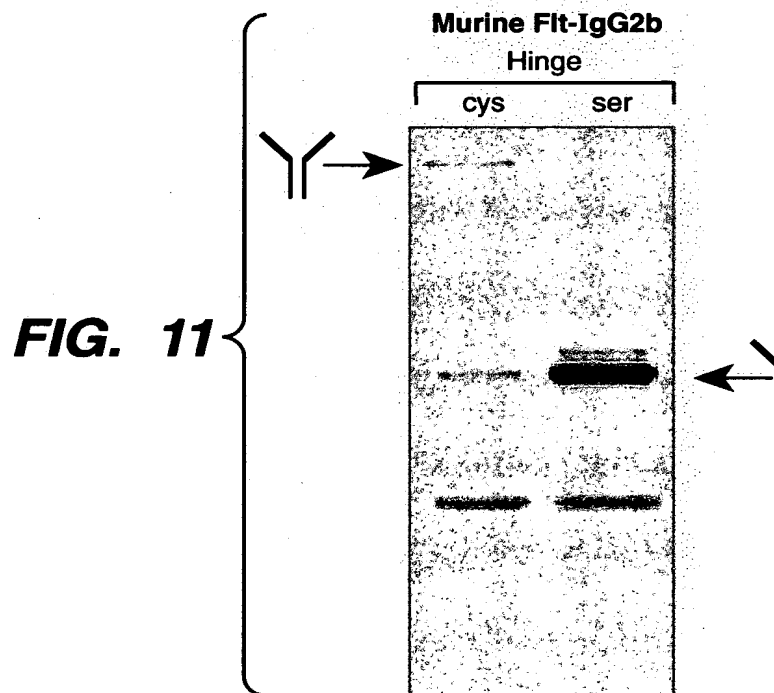
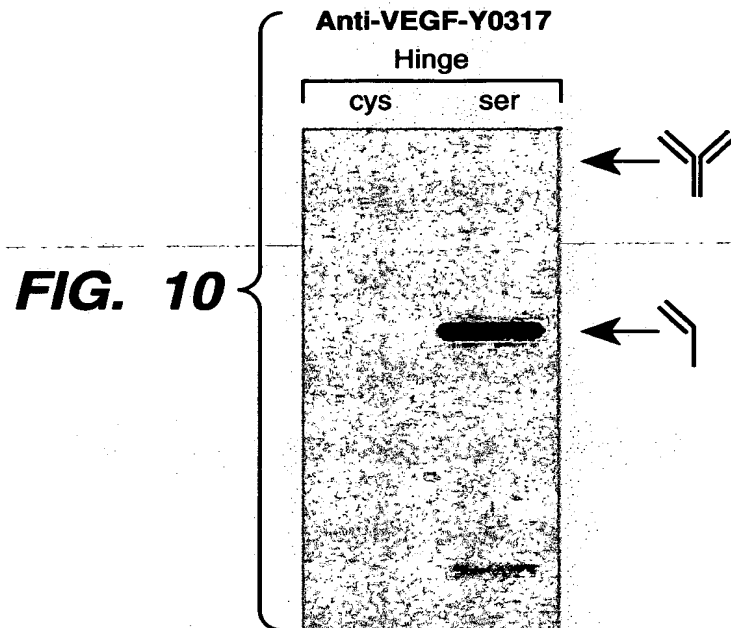
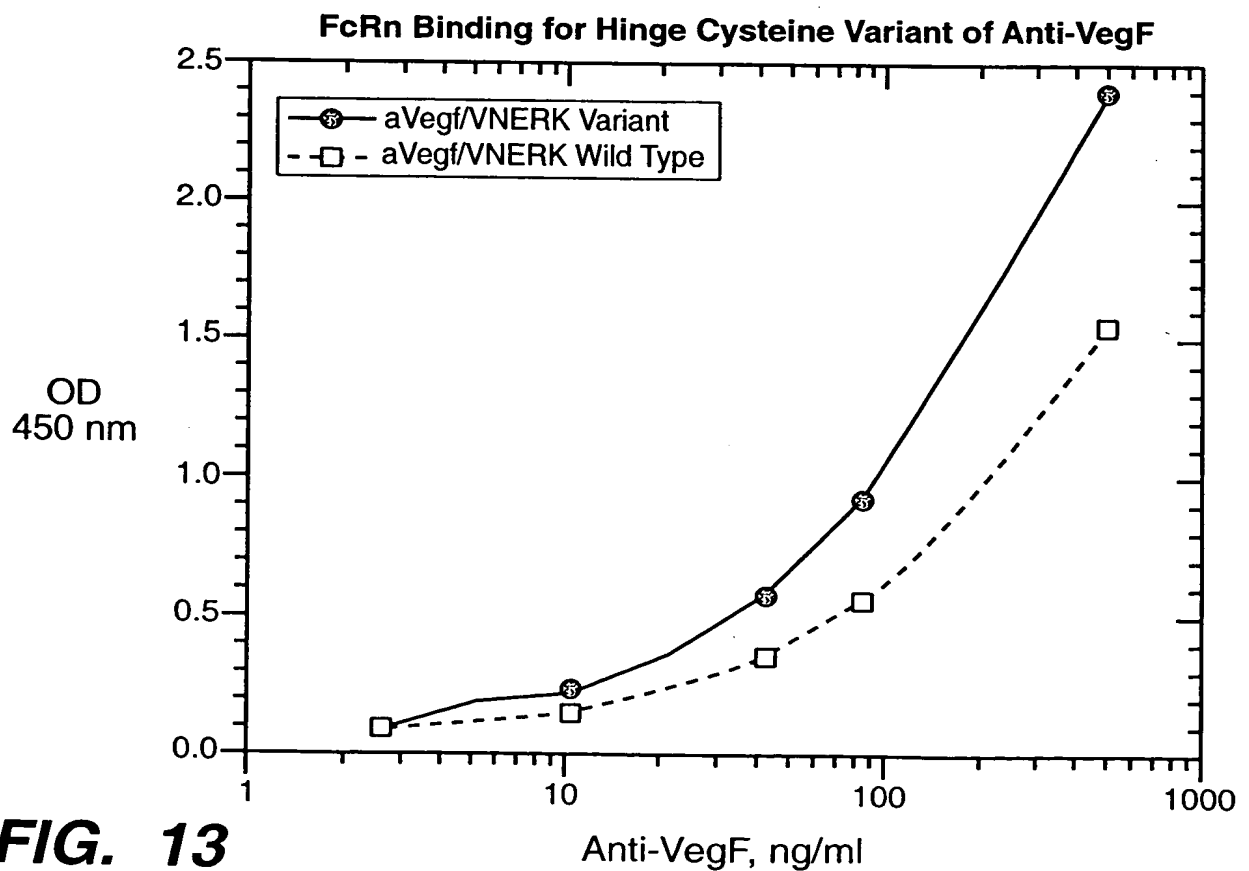
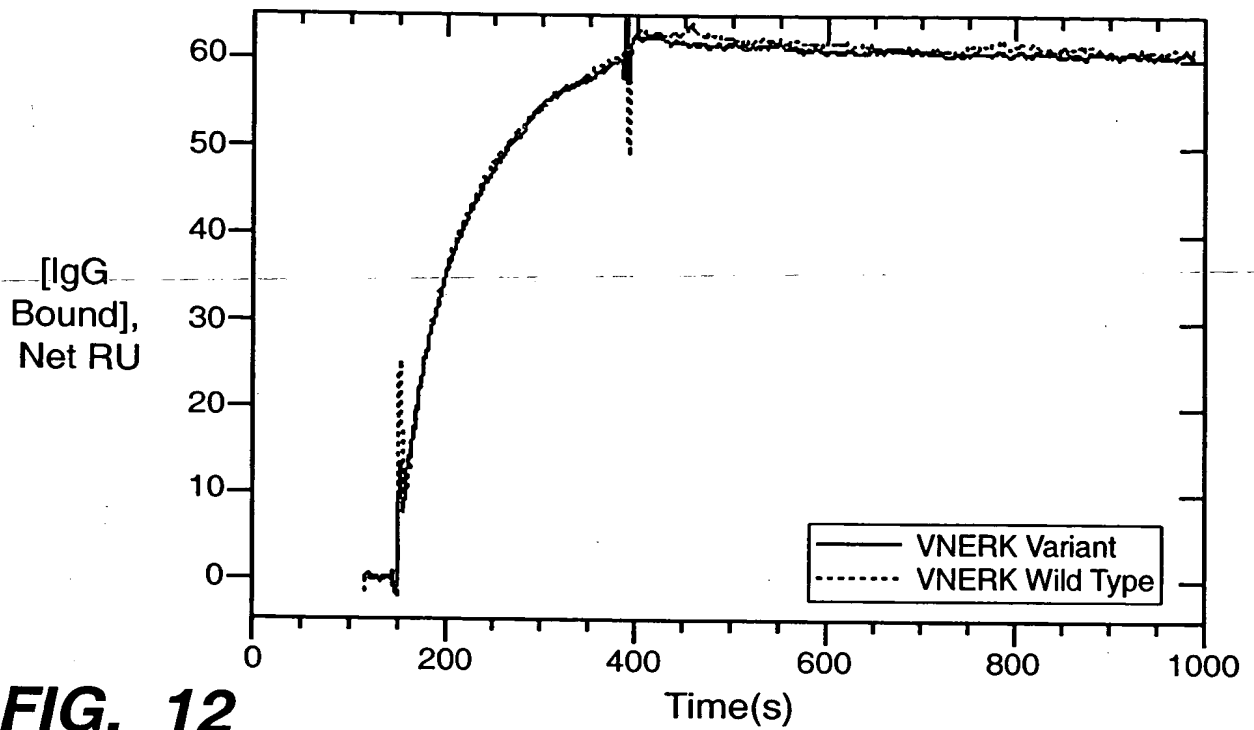


FIG. 9B





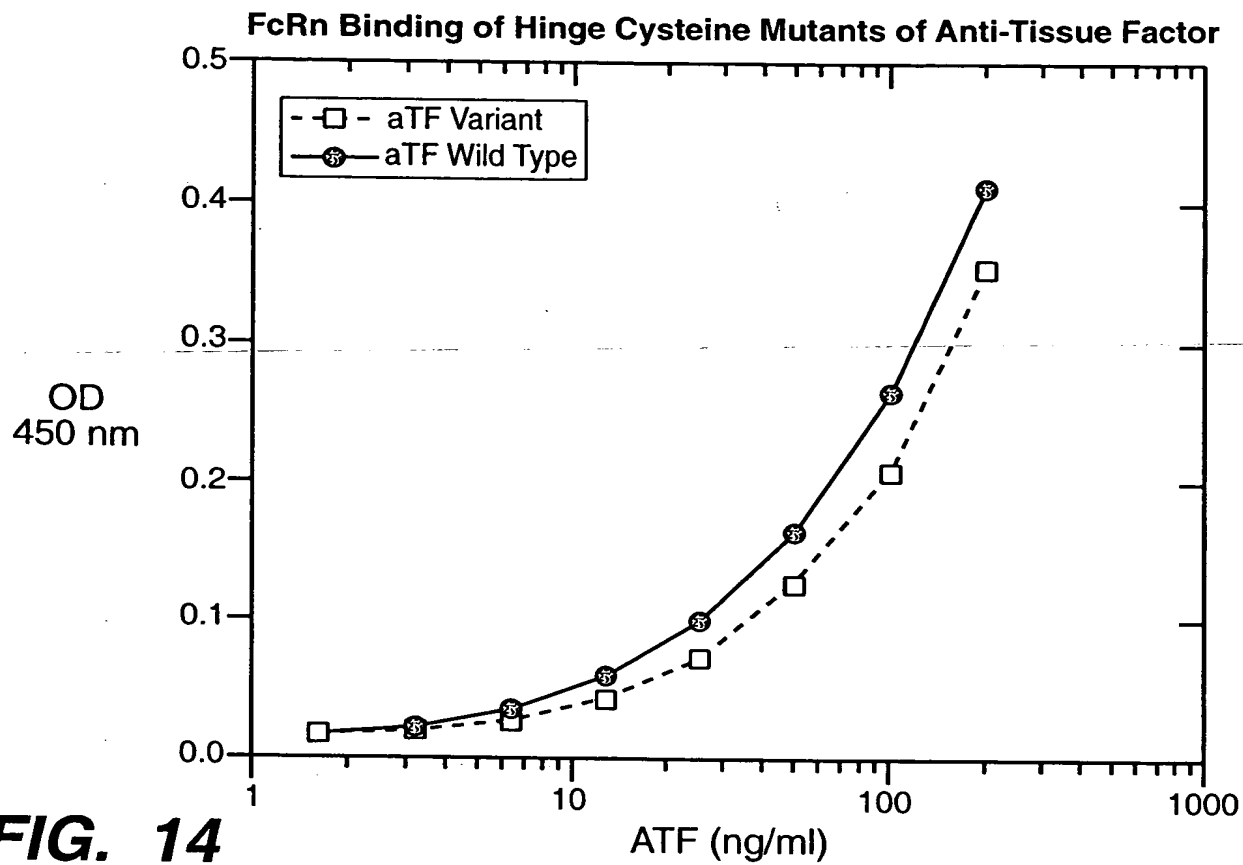


FIG. 14

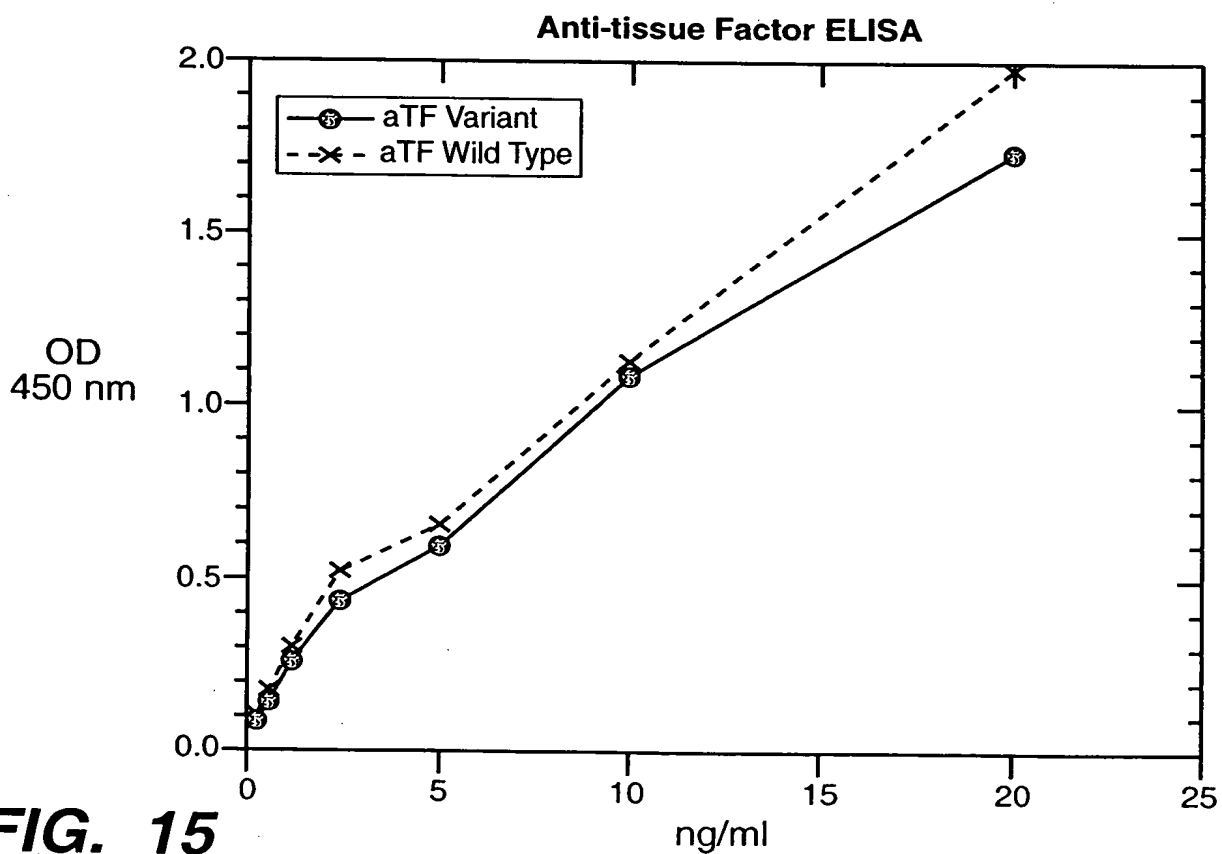
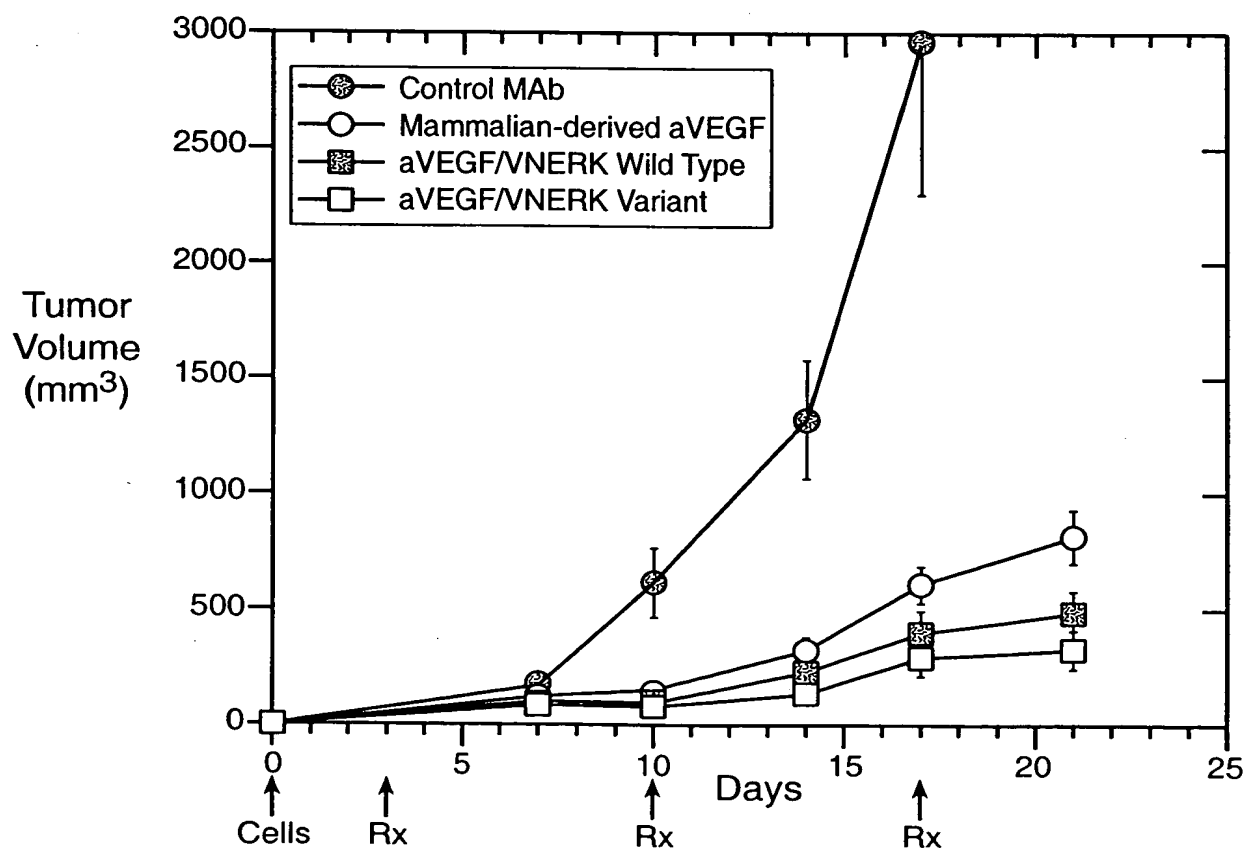
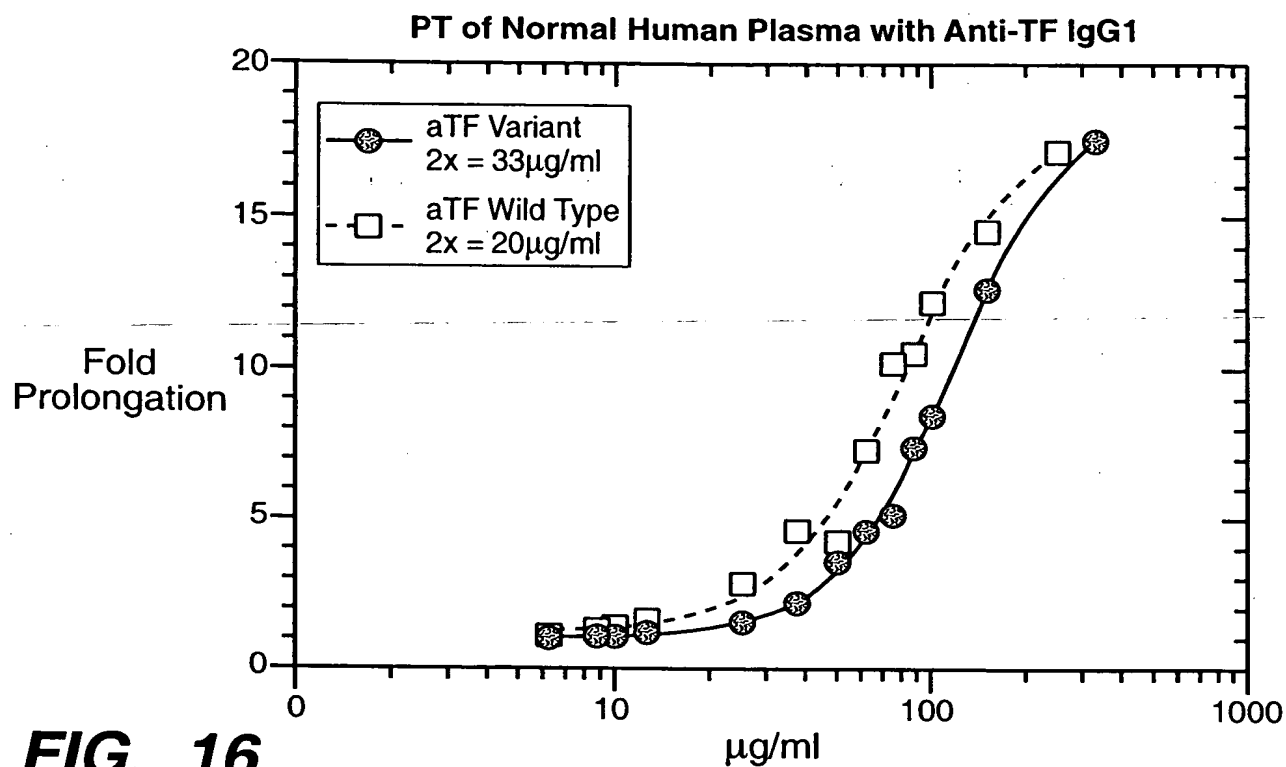


FIG. 15



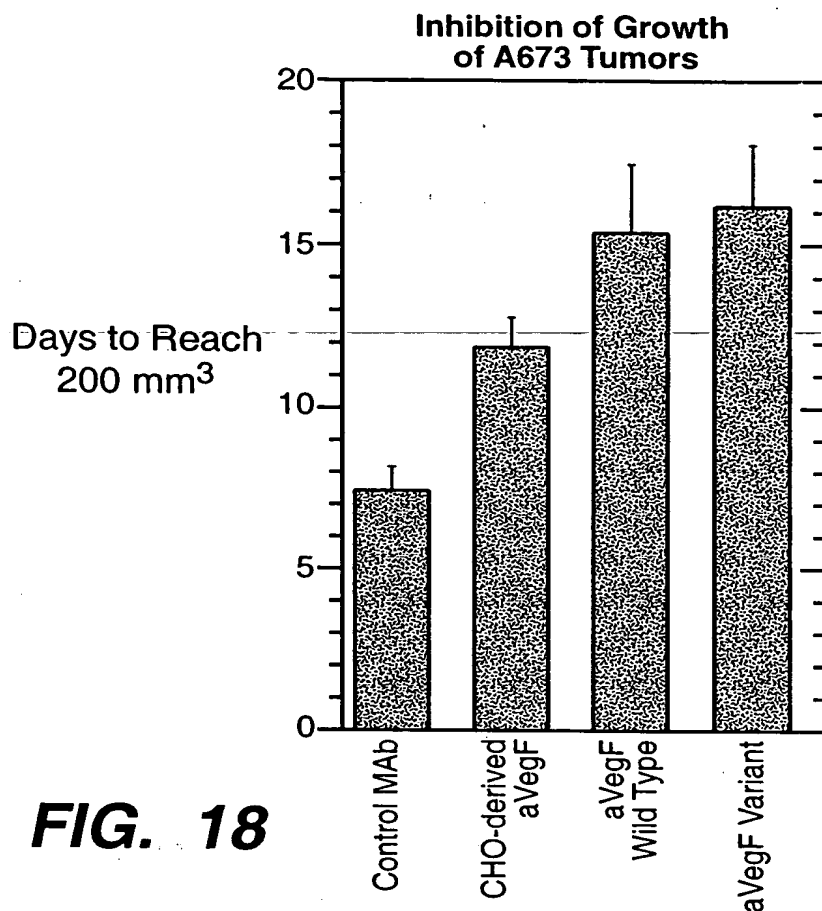


FIG. 18

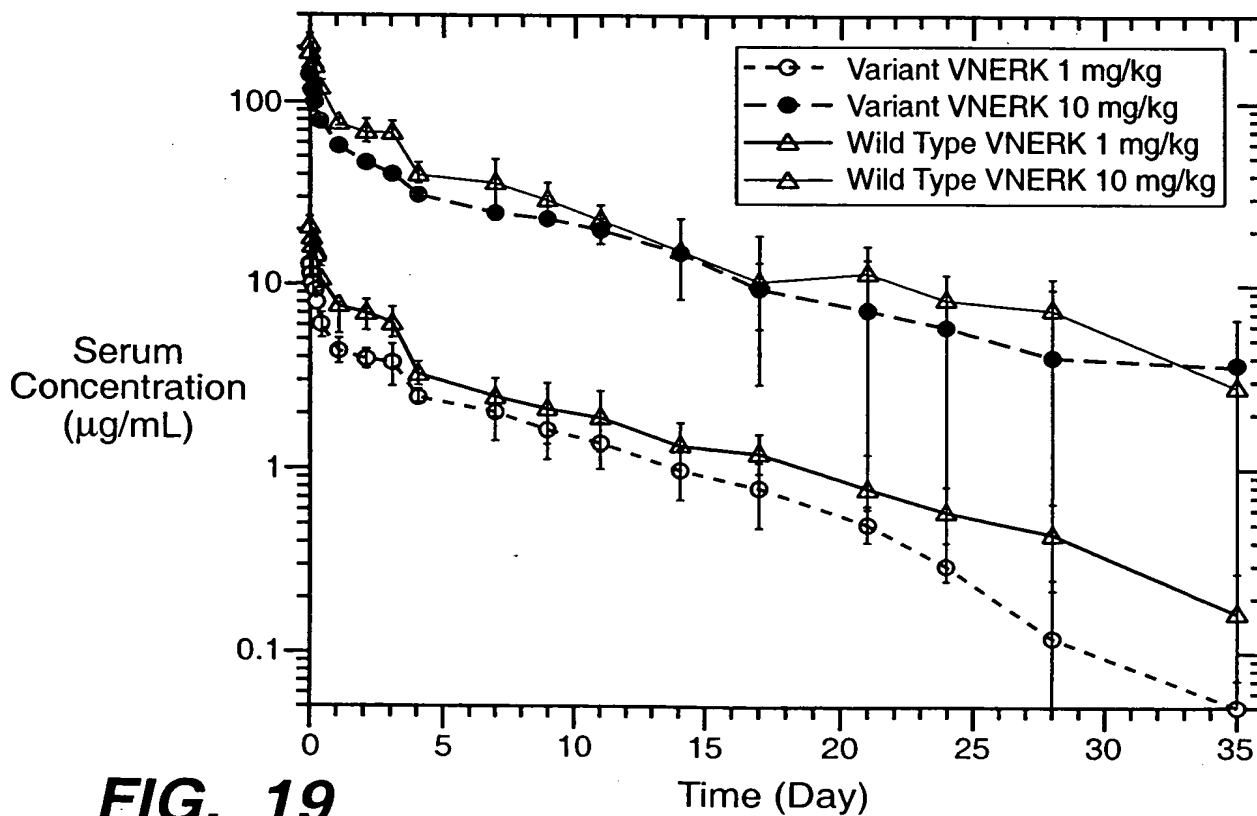


FIG. 19